

## STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 167420

TO: Lorraine Spector Location: 4d55 / 4c70

Monday, October 03, 2005

Art Unit: 1647

Phone: 571-272-0893

Serial Number: 09 / 674377

From: Jan Delaval

**Location: Biotech-Chem Library** 

Remsen 1a51

Phone: 571-272-2504

jan.delaval@uspto.gov

Search N		)t	es
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Rest 10/4/05



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#### STIC-Biotech/ChemLib

From:

Spector, Lorraine

Sent:

Friday, September 30, 2005 1:42 PM

To:

STIC-Biotech/ChemLib

Subject:

SEARCH request for Serial No. 09/674377

STIC,

Please search SEQ ID NO: 1 and 2

- -pending
- -issued
- -commercial

Also, please align the two sequences with each other.

Thanks.

Lorraine Spector
571-272-0893
U.S. Patent and Trademark Office
Art Unit 1647
lorraine.spector@uspto.gov
Office: Remsen 4D-55
Mailbox: Remsen 4C-70

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# STIC SEARCH RESULTS FEEDBACK FORM

#### Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

/oluntary Results Feedback Form
> I am an examiner in Workgroup: Example: 1610
Relevant prior art found, search results used as follows:
102 rejection
103 rejection
Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Drop off or send completed forms to STIC-Blotech-Chem Library Remsen Bldg



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   GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd
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158	158.5	159	182	186.5	189	192.5	195	204	217	225.5	228.5	230	235.5	260.5	268
6.1	6.1	6.1	7.0	7.2	7.3	7.4	7.5	7.8	8. <sub>3</sub>	8.7	8.8	8.8	9.0	10.0	10.3
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u-plasminogen acti	u-plasminogen acti	neurotrophic recep	hypothetical prote	plasma hyaluronan-	coagulation factor	plasma hyaluronan-	coagulation factor	hepatocyte growth	neurotrophic recep	t-plasminogen acti	coagulation factor	neurotrophic recep	ror-related recept	plasmin (EC 3.4.21	plasmin (EC 3.4.21

,	ALIGNMENTS
	RESULT 1 JH0579 hepatocyte growth factor precursor [validated] - human N;Alternate names: hepapoietin A; scatter factor
	C.Species: Homo sapiens (man) C;Dete: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004 C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33512; A39006; PH0114; A37796; S06 R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
	A;Title: Organization of the human hepatocyte growth factor-encoding gene. A;Reference number: JH0579; MUID:91340155; PMID:1831432 A;Accession: JH0579 A;Accession: JH0579 A;Accelsion: JNA
have a	A; Note: the authors translated the codon GAA for residue 662 as Glv A: Note: the authors translated the codon GAA for residue 662 as Glv
ŋ	R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S. submitted to JIPID, March 1991 A;Description: Organization of the human hepatocyte growth factor-encoding gene.
	A;Reference number: JU0333 A;Accession: JU0333 A.Molecule rune: NNA
	A;Residues: 1-481, 'RT', 484-728 <se2></se2>
ocyte growth	k; Weldner, K.M.; Arakaki, N.; Harrmann, G.; Vandekercknove, J.; Welngart, S.; Kreder, n. Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
ocyte growth	A;Title: Evidence for the identity of numan scatter factor and numan nepatocyte growth i A;Reference number: A41140; MUID:91334393; PMID:1831266
	A; Accession: A41140
phage-stimula phage-stimula	A;Residues: 1-728 <wbi></wbi>
phage-stimula	A,Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936  R.Goki T . Thara T . Sucimura A . Shimonishi M . Nishizawa T . Asami O . Haqiva N
) E	Biochem. Biophys. Res. Commun. 172, 321-327, 1990
in (EC 3.4.21 in (EC 3.4.21 in (EC 3.4.21	A;Ille: isolation and expression of construct different forms of departure growth fact. A;Reference number: A36677; MUID:91025062; PMID:2145836 A:Accession: B36677
in (EC 3.4.21	A; Molecule type: mRNA
otein(a) (EC	A;Cross-references: GB:M60718; NID:g184031; PIDN:AAA52648.1; PID:g184032 A;Accession: A36677
in (EC 3.4.21	A; Molecule type: mRNA A; Residues: 1-161,167-728 <se4></se4>
in precursor	A, Cross-references: EMBL:X16323
bin (EC 3.4.2)	A;Experimental source: leukocyte R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
bin (EC 3.4.2	Biochem. Biophys. Res. Commun. 163, 967-973, 1989
bin (EC 3.4.2	A;Ilie: Molecular cioning and sequence analysis of committee number neparocyte growing as A;Reference number: A33512; MUID:89392017; PMID:2528952
sminogen acti	A;Accession: A33512 A:Status: not compared with conceptual translation
sminogen acti	A; Molecule type: mRNA
III (EC 3:4:21	A; Residues: 1-/20 <pre></pre>

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A;Residues: 1-288, ET' <HAR>
A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A;Title: An alternatively processed mRNA generated from human hepatocyte A;Reference number: S15443; MUID:91200041; PMID:1826653
A;Accession: S15443
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084 R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K. Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991 A;Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibr A;Reference number: I52253; MUID:92062058; PMID:1835383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the authors translated the codon CAG for residue 727 as Glu A;Note: part of this sequence, including the amino end of both the alpha and beta R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growt A;Reference number: 159214; MUID:93087571; PMID:1280830
A;Accession: 159214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 86-91,329-344;356-363,'XX',366-370;425-434,442-447,'X',449-450;543-546,'R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Nature 342, 440-443, 1989
A;Title: Molecular cloning and expression of human hepatocyte growth factor.
A;Reference number: S06794; MUID:90066676; PMID:2531289
A;Accession: S06794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 37-43;53-58 <70S>
A;Experimental source: plasma
R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier,
J. Cell Biol. 111, 2097-2108, 1990
A;Title: Scatter factor: molecular characteristics and effect
A;Reference number: A37796; MUID:91035621; PMID:2146276
A;Accession: A37796
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                                                                                                                      A;Map position: 7g21.1-7g21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; C;Complex: disulfide-bonded heterodimer of chains derived
                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 161-166 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: I52253
A;Status: preliminary; translated
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A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
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                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:S62561; NID:g237996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-288, 'ET' <MIY2>
                                                              A; Description: stimulates mitosis of hepatocytes and other
                                                                                             C; Function:
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      ;Superfamily:
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                                                                                                                                                                                                              Cross-references: GDB:127524; OMIM:142409
                                  does not
   hepatocyte growth
                            have
   growth
activity
factor/macrophage
                                                                                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
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   stimulating protein
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                                                                                                                         347/2; 390/1; 424/2; 469/1; from the same precursor
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                                                                                                                                      R;Rosen,
                                                           A; Molecule type: protein
A; Residues: 496-504 <SA2>
                                                                                                                                                                                                                                                                                                  A;Reference number: JC2117; MUID:94183257; PMID:8135822
A;Accession: JC2117
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E.M.; Meromsky, c. Exp. Biol. Mer

Med. ۲.

195, Setter, 34-43,

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D.W.;

Goldberg,

NID:g220435;

PIDN:BAA01064.1;

PID:g220436

I48758;

JU0231

factor

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C;Keywords: alternative splicing; glycoprotein; growth fact F;1-31/Domain: signal sequence #status predicted <SIO> F;32-494,495-728/Product: hepatocyte growth factor #status F;32-494/Domain: alpha chain #status experimental <ACH> F;128-206/Domain: kringle homology <KR1> F;211-288/Domain: kringle homology <KR2> F;311-288/Domain: kringle homology <KR3> F;301-469/Domain: kringle homology <KR4> F;391-469/Domain: kringle homology <KR4> F;391-469/Domain: kringle homology <KR4> F;391-469/Domain: kringle homology <KR4> F;391-469/Domain: beta chain #status experimental <BCH> F;495-728/Domain: beta chain #status experimental <BCH> F;495-728/Domain:
hepatocyte growth factor precursor - mouse
N;Alternate names: hepapoietin A; Scatter factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: JC2117; PC2064; A60185; 843416; S45521; S17173; S10986; I48758
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
Biochem. Biophys. Res. Commun. 199, 772-779, 1994
A;Title: Identification of mouse mammary fibroblast-derived mammary growth
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F;32/Modified site: pyrrolidone carboxylic acid
F;32/Modified site: carbohydrate (As
F;294,402;566,653)Binding site: carbohydrate (As
F;487-604/Disulfide bonds: #status predicted
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Pred. No. 1.9e-176;
1; Mismatches 0;
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d <SIG>
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n) (covalent) #status predicted
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A;Note: does not have proteinase activity

C;Superfamily: hepatocyte growth factor/macrophage stimulating pr
C;Keywords: alternative splicing; glycopretein; growth factor; he
F;1-3z/Domain: signal sequence #status predicted <SIG>
F;56-495,496-728/Product: hepatocyte growth factor #status predicter;
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicter;
F;209-207/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: kringle homology <KR4>
F;496-719/Domain: kringle homology <KR4>
F;496-719/Domain: kringle homology <KR4>
F;496-719/Domain: kringle homology <KR4>
F;496-719/Domain: krypsin homology <KR4>
F;496-719/Domain: krypsin homology <KR4>
F;496-719/Domain: krypsin homology <KR4>
F;496-719/Domain: krypsin homology <KR4+
F;496-719/Domain: krypsin homolog
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A;Accession: $45521
A;Status: preliminary
A;Molecule type: mRN/
A;Residues: 1-563,'H
A;Cross-references: 1
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A;Title: Purification and characterization of biologically active A,Reference number: S17173; MUID:91354223; PMID:1831975
A;Accession: S17173
A;Molecule type: nyothing
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A;Reference number:
A;Accession: S10966
A;Accession: orelimina
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A;Molecule type: mRNA
A;Residues: 1-728 <LIU>
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Biochim. Biophys. Acta 1216, 299-303, 1993
A;Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte & A;Reference number: S43416; MUID:94060105; PMID:8241272
A;Accession: S43416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residus: 1-30 (RES)
A;Cross-references: EMBL:X81630; NID:g673451; PIDN:CAA57286.1; PID:g673452
C;Complex: disulfide-bonded heterodimer of chains derived from the same pre
C;Function:
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
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A;Molecule type: protein
A;Molecule type: protein
A;Residuss: 496-507,'X',509-512,'L',514-516,'X',518-519 <NAT>
A;Residuss: 496-507,'X',509-512,'L',514-516,'X',518-519 <NAT>
B;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W
J. Biol. Chem. 270, 830-836, 1995
J. Biol. Chem. 270, 830-836, 1995
A;Title: Characterization of the scatter factor/hepatocyte growth
A;Reference number: 148758; MUID:95122532; PMID:7822318
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R;Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
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Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homoly, Superfamily: hepatocyte growth factor; heterodimer; kringle; py Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; py 1-32/Domain: signal sequence #status predicted <SIG>
15-495/496-728/Product: hepatocyte growth factor #status predicted <ACH>
15-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
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:Reference number: A60185; MUID:90377927; PMID:2144630
Accession: A60185
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Residues: 1-563,'H',565-728
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66; MUID:90326152; PMID:2142751
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21; Mismatches
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              CYTGNPLIPWDYCPISRCEGDTTPTIV 447
                                                                                                         QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCUVSSGQDC
                                                                                                                        QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                                                                                                                                            YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                                                                                                                   MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
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CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                     YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW
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N; Alternate I C; Species: R; C; Date: 28-S; C; Accession: C;Date: 28-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_chac;Accession: A35644; S13211
R;Tashiro, K; Hagiya, M; Nishizawa, T.; Seki, T.; Shimonis Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth A;Reference number: A35644; MUID:90222197; PMID:2139229
A;Accession. A35644 A;Cross-references: UNIPROT:P17945; GB:D90102; GB:M32987; NID:g220766; PIDN:BAA14133 A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 7 A; Molecule type: mRNA A; Residues: 1-728 < TAS> hepatocyte growth factor epatocyte growth factor precursor - rat; Alternate names: hepapoietin A; scatter factor; Species: Rattus norvegicus (Norway rat) T.; Shimonishi, M.; Shimizu, #text\_change 09-Jul-2004 and expression ა : Nakamur of the

Status: preliminary

R;Okajima, A.; Miyazawa, K.; Kitamura, N. Eur. J. Biochem. 193, 375-381, 1990 A;Tille: Primary structure of rat hapatocyte growth factor A;Reference number: S13211; MUID:91031482; PMID:2146117 and induction of. 100

A;Reference number: S13211; MUID:91031482; PMID:2146117
A;Accession: S13211
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-728 <OKA>
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same pro precursor

1; kringle homold
imer; kringle; pyr

A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle hc;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle f;1-3/Domain: signal sequence #status predicted <SIGO
F;56-495/Domain: hepatocyte growth factor #status predicted <MAT>
F;56-495/Domain: kringle homology <KR1>
F;129-207/Domain: kringle homology <KR1>
F;129-207/Domain: kringle homology <KR2>
F;303-384/Domain: kringle homology <KR3>
F;302-470/Domain: kringle homology <KR4>
F;496-719/Domain: kringle homology <KR4>
F;496-719/Domain: kringle homology <KR4>
F;496-719/Domain: krypsin homology <KR4>
F;496-719/Domain: trypsin homology <KR4>
F;496-719/Domain: trypsin homology <KR4>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted

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A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; k
C;Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle
F;42-477,478-709/Product: hepatocyte growth factor #status predicted <MAT>
F;42-477/Domain: hepatocyte growth factor alpha chain #status predicted <AC
F;115-193/Domain: kringle homology <KR1>
F;198-275/Domain: kringle homology <KR2>
F;289-367/Domain: kringle homology <KR3>
F;375-453/Domain: kringle homology <KR4>
F;375-453/Domain: kringle homology <KR4>
F;478-700/Domain: hepatocyte growth factor beta chain #status predicted <BC
F;478-709/Domain: trypsin homology <KR4>
F;478-709/Domain: trypsin homology <KR4
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A;Molecule type: mRNA
A;Residues: 1-411 <STR>
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  CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT
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Best Local Similarity Matches 305; Conserv
                                                                                                                                                                                                                                                                                                                 CNGESYRGIMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT
                                                                                                                                                                                                                                                                                                                                                                              SMIPHEHSFLPSTYRGKDLKENYCRNPKGEEGGPWCFTKSPEVRHDVCDIPFCSEVDCVT
                                                                                                                                                                                                                                                                                                                                                                                                  SMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS
                                                               GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCY
                                                                                                                                                  PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR
                                                                                                                                                                                                           LDPDTSWEFCAIKPCVHSIVNNTDI---
                                                                                                                                                                                                                                   LDPHTRWEYCAIKTCADNIMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY
                                                                                                                                                                                                                                                                                           CNGEHYRGPMDYTESGKECQRWDLQRPHKHKFRPERYPNKGLNDNYCRNPDGKSRPWCYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKRNAFDDYKKTAETTLTRLNKALEVKTKMFNTTENCAKRCSRNKGLPFTCKAFAFDKNI
TGNPLIPWDYCPISRCEGDT
                                         GNGSTYKGTLSRTRFRLPCSMWEKNLQDLKRHTFNEPDVSILQKNYCRNPDNDAHGPWCY
                                                                                                                          PHLHNFTPENYKCKDLSENYCRNPDGSESPWCFTTDPNIRIGHCSQIKKCQASNQQECYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR
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4; Mismatches 68;
    442
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R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Ap Development 121, 813-824, 1995
A;Title: A role for HGF/SF in neural induction and its A;Reference number: I51285; MUID:95237013; PMID:7720585
A;Accession: I51285 hepatocyte growth factor/scatter factor - chicken (C;Species: Gallus gallus (chicken) (C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 (;Accession: I51285 R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W. A;Cross-references: UNIPROT:Q90978; GB:S77480; NID:g998675; PID:g998676 C;Superfamily: hepatocyte growth factor/macrophage stimulating protein: F;124-197/Domain: kringle homology <KRGs F;202-279/Domain: kringle homology <KR2> F;296-374/Domain: kringle homology <KR3> translated from GB/EMBL/DDBJ chicken (fragment) G.W.; Aparicio, #text\_change expression : : 09-Jul-2004 Ľ, Sharpe, M.J.; Hensen's kringle

node

durin

homo

Gherard

KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR KRCHWLSFNSLTNGVRKKQDHAFDLFEKKDYVRNCIIGKGAEYKGTISITKSGIQCQAWN KRRNPLHDYKKTGELMLIKVNKTLEVKTKLLNTTEQCAKRCSRNKGLSFTCKAFAYDRVT SMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 66.7%; 74.9%; 47; Score 1737.5; DB 2, Pred. No. 1.3e-115; 7; Mismatches 45; 2; Length PLCSEVECMT 5 182 149 122 89 204

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A,Gene: GDB:MSTI; D3F15S2; DNF15S2; HGFL
A,Gene: GDB:MSTI; D3F15S2; DNF15S2; HGFL
A,Cross-references: GDB:128833; OMIM:142408
A,Cross-references: GDB:128833; OMIM:142408
A,Map position: 3p21-3p21.3
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; Kringle homolc C;Keywords: duplication; glycoprotein; growth factor; kringle; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-483,484-711/Product: macrophage-stimulating protein 1 #status predicted <MAT>
F;19-483/Domain: alpha chain #status predicted <ACH>
F;110-186/Domain: kringle homology <KR1>
F;12-368/Domain: kringle homology <KR2>
F;283-361/Domain: kringle homology <KR3>
F;484-701/Domain: kringle homology <KR3>
F;484-701/Domain: beta chain #status predicted <BCH>
F;484-701/Domain: trypsin homology <TRY>
F;56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37
F;72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macrophage-stimulating protein 1 precursor - human
C;Species: Homo sapiens (man)
C;Cpecies: User (man)
C;Cpecies: Homo sapiens (man)
A;Title: Characterization of the DNF1552 locus on human chromosome 3: identification
A;Title: Characterization (man)
A;Title: Characterization (man)
A;Residues: 1-711 <HA1>
A;Ccossion: H40331
A;Accession: H40331; MUID:92002016; PMID:1655021
A;Accession: H40331
A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A61395
A;Molecule type: protein
A;Residues: 230-247;288-291,'E',
A;Experimental source: plasma
C;Genetics:
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197; Conser
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      Conservative
                               45.3%;
      62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293-295, 'X', 297-301, 'X', 303, 'E', 305, 'EX', 308-310; 326-33
Score 1180.5; DB 1;
Pred. No. 5.6e-76;
2; Mismatches 148;
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C;Date: 31-
C;Accession
R;Ohshiro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P70521; EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; PII C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle rC;Keywords: duplication; glycoprotein; growth factor; kringle r;1-31/Domain: signal sequence #status predicted <SIG- r;32-488 /489-716/Product: macrophage-stimulating protein 1 #status predicted <ACF;110-186/Domain: kringle homology <KRI1- r;191-268/Domain: kringle homology <KRI2- r;191-268/Domain: kringle homology <KRI2- r;292-370/Domain: kringle homology <KRI3- r;399-457/Domain: kringle homology <KRI4- r;379-457/Domain: kringle homology <KRI4- r;399-716/Domain: kringle homology <KRI4- r;399-716/Domain: kringle homology <KRI4- r;489-716/Domain: krypsin homology <KRI4- r;4
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A;Title: Molecular cloning of rat macrophage-stimulating A;Reference number: JC5061, MUID:97011126; PMID:8858136
A;Accession: JC5061
A;Molecule type: mRNA
A;Residues: 1-716 < OHS>
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C;Species: Rattus norvegicus (Norway rat)
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   PRGPWCYTTNRSVRFQSCGIKSCREAVCVWCNGEDYRGEVDVTESGRECQRWDI
                                                              EGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH
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                                                                                                                                YVRTCIMDNGASYRGTVARTADGLPCQAWSRRFPNDHKYTPTPKNG--LEENFCRNPDGD
                                                                                                                                                                                              YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE
                                                                                                                                                                                                                                                                   VADAEECARRC---
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Pred. No. 2.1e
70; Mismatches
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protein 1; kringle homolo
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F;1-31/Domain: signal sequence #status predicted <SIG>
F;19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
F;19-483/Domain: alpha chain #status experimental <ACH>
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C; Complex: disulf
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A;Title: Characterization of the mouse cDNA and gene coding A;Reference number: A40332; MUID:92002017; PMID:1832957
A;Accession: A40332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;110-186/Domain: kringle homology <KR1>F;111-268/Domain: kringle homology <KR2>F;292-370/Domain: kringle homology <KR3>F;379-457/Domain: kringle homology <KR4>F;379-457/Domain: kringle homology <KR4>F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolc C;Keywords: duplication; glycoprotein; growth factor; kringle
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A; Residues: 1-18,'P',20-716 < DEG2 >
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A; Residues: 1-716 < DEG>
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                                                                                                                                                           YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE
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   PRGPWCYTTNRSVRFQSCGIKTCREAVCVLCNGEDYRGEVDVTESGRECQRWDLQHPHSH
                                                   EGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH
                                                                                                                       YVRTCIMDNGVSYRGTVARTAGGLPCQAWSRRFPNDHKYTPTPKNG--LEENFCRNPDGD
                                                                                                                                                                                                                                           VADAEECARRC----GPLLDCRAFHYNMSSHGCQLLPWTQHSLHTQLYHSSLCHLFQKKD
                                                                                                                                                                                                                                                                                                         VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD
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                                                                                                                                                                                                                                                                                                                                                                      Score 1125; DB 1; Length 716;
Pred. No. 4.7e-72;
9; Mismatches 143; Indels 1
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                                             A; Pathway: fibrinolysis
C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F; 1-790/Product: plasminogen #status predicted <PRO>
F; 1-77/Domain: activation peptide #status predicted <APT>
F; 1-77/Domain: activation peptide #status predicted <APT>
F; 18-560/Product: plasmin chain A #status predicted <ACH>
F; 184-162/Domain: kringle homology <KR1>
F; 84-162/Domain: kringle homology <KR2>
F; 156-333/Domain: kringle homology <KR3>
F; 156-333/Domain: kringle homology <KR3>
F; 556-333/Domain: kringle homology <KR3>
F; 556-390/Product: miniplasminogen #status experimental <MIN>
F; 461-540/Domain: kringle homology <KR8>
F; 561-783/Domain: kringle homology <KR8>
F; 561-783/Domain: kringle homology <KR9>
F; 561-783/Domain: kringle homology <KR9-297, 187-226, 215-238, 256-333, 277-316, 305
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R,Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M. Bur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Recession: S03737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-57 <BRU'>
R;Marri, T.; Schaller, J.; Rickli, E.E.

Eur. J. Biochem. 149, 279-285, 1985
Eyr. J. Biochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence
A;Reference number: A25834; MUID:85203907; PMID:3846533
A;Accession: A25834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence-vision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S03733; S03737; Ā25834
R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparia, Reference number: S03733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-560 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S03733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Contains: miniplasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmin (EC 3.4.21.7) precursor - N;Alternate names: plasminogen
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F;602,645,740/Active site: His,
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A;Description: dissolves the fibrin of blood clots; acts as a proteolytic ns the walls of the graafian follicle; also activates the urokinase-type p A;Pathway: fibrinolysis C;Superfamily: plasmin: Princip Learning
                                                                                                         C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasm mediately after dissociation from the clot. In the presence of the inhibitor, the activation involves also removal of the activation peptide. C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. eful in treating solid tumors.
                                                                                                                                                                                                                                      Eur. J. Biochem. 224, 863.871, 1994
A;Title: Characterization of the murine plasma fibrinolytic A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIJ>
A;Accession: S48203
A;Molecule type: protein
A;Residues: 22-27 <LIZ>
                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-812 <DEG>
A; Cross-references: UNIPROT: P20918; GB: J04
R; Lijnen, H.R.; van Hoef, B.; Beelen, V.;
Bur: J. Biochem. 224, 863-871, 1994
Eur: J. Biochem. 224, 863-871, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence revision 01-Nov-1996 #text_change
C;Accession: A38514; S48202; S48203
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A;Ritle: Characterization of the cDNA coding for mouse plasminog
A;Reference number: A38514; MUID:91184812; PMID:2081600
A;Accession: A38514
                                                                  eful in treating C; Function: A; Description: d
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVLFEKRIYLSECKTGNGKNYRGTTSKTKSGVICQKWSVSSPHIPKYSPEKFPLAGLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTGNPLIPWDYCPISRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPDGSESPWCFTTDPNIRVGYCSQIPNCDMS----H---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRW
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Pred. No. 7.8e
65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:J04766; NID:g200402; n, V.; Collen, D.
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  precursor
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                                           plasminogen
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F;97-581,582-812/Product: plasmin #status predicted <ACH>
F;97-581/Domain: chain A #status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;105-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR4>
F;481-560/Domain: chain B #status predicted <BCH>
F;582-812/Domain: trypsin homology <TRY>
F;49-37,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,
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F;20-96/Domain: activation peptide #status predicted <APT>
F;79-466/Product: angiostatin #status predicted <AST>
F;97-581,582-812/Product: plasmin #status predicted <MAT>
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Best Local S
Matches 191
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                                    LIPWDYCPISRCEGDTTPTIV
SVRWEYCNLKRC-SETGGSVV
                                                                             GTSSTTITGKKCQSWAAMFP--HRHSKTPENFPDAG-LEMNYCRNPDGD-KGPWCYTTDP
                                                                                                                    GNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNP
                                                                                                                                                                DGETAPWCYTTDSQLRWEYC-EIPSCESSASPDQSDSSVPPEEQTPVVQECYQSDGQSYR
                                                                                                                                                                                                       DGSESPWCFTTDPNIRVGYCSQIPNCDMSHG-----
                                                                                                                                                                                                                                                  PPSPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEENYCRNP
                                                                                                                                                                                                                                                                              VPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNP
                                                                                                                                                                                                                                                                                                                                QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCOPWSSMIPHEHSFLPSSYRGKDLQENYC
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Pred. No. 2.5e-67;
7; Mismatches 145
                                                                                                                                                                                                                                                                                                                                                                                                                    -ECMYCSGEKYEGKISKTMSGLDCQAWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145;
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plasmin (EC 3.4.21.7) precursor - western European hedgehog C;Species: Erinaceus europaeus (western European hedgehog) C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change C;Accession: 146260 R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, J. Biol. Chem. 270, 24004-24009, 1995 A;Title: The recurring evolution of Lp(a): Insights from cloning A;Reference number: 146259; MUID:96025778; PMID:7592597 A;Accession: 146260 A;Steatus: prellaminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA

Insights from cloning PMID:7592597

of hedgehog D.P.;

apolipopro . Fon

Byrne,

09-Jul-2004

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RESULT 12
B30848
B30848
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989
C;Accession: B32869; B30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence,
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A;Cross-references: UNIFROT:029485; EMBL:U33171; NID: C;Superfamily: plasmin; kringle homology; plasminogen C;Keywords: hydrolase; serine proteinase F;1-96/Domain: plasminogen-related protein precursor F;103-181/Domain: kringle homology <KR1>F;185-262/Domain: kringle homology <KR3>F;275-552/Domain: kringle homology <KR3>F;379-456/Domain: kringle homology <KR4>
                                                       A;Residues: 1-810 <TOM>
A;Rossidues: 1-810 <TOM>
A;Cross-references: UNIPROT:P12545; GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g34227: A;Cross-references: UNIPROT:P12545; GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g34227: C;Superfamily: plasminy kringle homology; plasminogen-related protein; hydrolase; kringle; serine proteinase F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-9/Domain: signal sequence status predicted <SIG>
F;1-9/Domain: kringle homology <KR1>
F;1-8/Domain: kringle homology <KR2>
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                  F;275-352/Domain:
F;377-454/Domain:
                                                                                                                                                                                                               A; Molecule type: mRNA
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582-803/Domain:
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trypsin
kringle homology <KR3>
kringle homology <KR4>
kringle homology <KR5>
                                                    kringle homology <KRl>
kringle homology <KR2>
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Pred. No. 6.1e
53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            31-Mar-1989
                                                                                                                                                                                                                                                                              Sequence, evolution, PMID:2925643
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-810 <PET>
A; Residues: 1-810 <PET>
A; Residues: 1-810 <PET>
A; Cross-references: UNIPROT: P00747; UNIPROT: Q9UBQ9; UNIPROT: Q9UMI2
A; Experimental source: leukocyte; lung fibroblast
A; Experimental source: leukocyte; lung fibroblast
A; Experimental source: leukocyte; lung fibroblast
A; Candiani, G.; Meroni,
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A; Title: Definition of the transcription initiation site of human
A; Reference number: I52242; MUID: 91097523; PMID: 2268308
A; Accession: I52242; FORMET, NDR.T
                                                                                                                                                                                                         plasmin (EC 3.4.21.7) precursor [validated] - human
N.Alternate names: plasminogen precursor [misnomer]
N.Contains: angiostatin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Ju
C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929;
C:Accession: A35229; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A;Title: Characterization of the gene for human plasminogen, a key pr
A;Reference number: A35229; MUID:90202879; PMID:2318848
A;Accession: A35229; MUID:90202879; PMID:2318848
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F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
bonds: #status predicted
F;622,665,760/Active site: His, Asp, Ser #status predicted
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A; Status: translated from GB/EMBL/DDBJ
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42.6%;
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0929; A04627;
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                                                              plasminogen gene
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A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810
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A; Residues: 367-419 < MAL3>
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;Residues: 292-471,'D',473-810 <MAL2>;Cross-references: GB:K02922; NID:g190112; 
;Accession: I84609
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Cross references: GB:X05199; NID:g35530; PIDN:CAA28831.1;
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A;Reference number: $43645; MUID:94237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
A;Rejante, M.R.; Llinas, M.
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A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasmin A;Reference number: A58817; MUID:94237158; PMID:8181476
A;Reference number: A58817; MUID:94237158; PMID:8181476
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A;Title: Crystal and molecular structure of human plasminogen A;Reference number: A58819; MUID:92031502; PMID:1657148
  A;Contents: annotation; conformation by (1)H-NMRC;Comment: Plasminogen is synthesized by the kidtC;Comment: Plasminogen is converted to plasmin by
                                                                                                                                                                                                                                                                                                                                            submitted to the Brookhaven Protein Data A;Reference number: A65804; PDB:IHPK A;Contents: annotation; conformation by
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A;Title: Kringle domains of human angiostatin.
A;Reference number: A58811; MUID:97067211; PMI
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F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: dissolves the ns the walls of the graafian A;Pathway: fibrinolysis
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A;Introns: 17/1; 62/2; 98
C;Function:
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                                     plasmin (EC 3.4.21.7) precursor - N;Alternate names: plasminogen
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   C;Species: Bos
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                                                                                                                                                                                                                                                        DPSVRWEYCNLKKCSG-TEASVV
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F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583,584-812/Product: plasmin #status experimental <AMT>
F;104-583/Domain: plasmin chain A #status experimental <ACH>
F;104-583/Domain: kringle homology <KR1>
F;102-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR2>
F;284-461/Domain: kringle homology <KR4>
F;384-461/Domain: kringle homology <KR4>
F;384-661/Domain: kringle homology <KR4>
F;485-564/Domain: kringle homology <KR4>
F;485-564/Domain: kringle homology <KR5>
F;486-805/Domain: kringle homology <KR5>
F;584-812/Domain: blasmin chain B #status experimental <BCH>
F;584-805/Domain: blasmin c
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A;Residues: 706-743, "K, "745-812 <MAL>
A;Residues: Toforences: GB:KO2935; NID:g163551; PIDN:AAA30714.1; PID:g163552
A;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Mann Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03735
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C;Accession: S45046; A25835; I45961; S03736
R;Berglund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A;Description: Cloning and characterizatin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: liver
A;Note: it is uncertain whether Met-1 or Met-8
R;Schaller, J.; Moser, P.W.; Dannegger-Muller,
Eur. J. Biochem. 149, 267-278, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: plasmin; kringle homology; plasminogen-related p
C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase;
F;1-26/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: dissolves the ns the walls of the graafian
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A; Residues: 27-83 < BRU>
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A; Residues: 27-334,'D',336-515,'H',517-554,'L'
A; Residues: 27-334,'D',336-515,'H',517-554,'L'
R; Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete amino acid sequence of bovine plasminogen. A;Reference number: A25835; MUID:85203906; PMID:3846532 A;Accession: A25835
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A; Residues: 1-812 <BER>
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A; Accession: S45046
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Matches
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FDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQEN 144
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Pred. No. 7.
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Oy 198 GKI Db 2609 GQP Qy 258 ADN CY 2669 -ES Db 2728 LFG CY 370 GNL CY 427 LIP CY 427 LIP	Ouery Match Best Local Simi Authors 173;  Authors 2490 EPL Db 2490 EPL Db 2490 EPL Db 2550 PDG	RESULT 15 T18518 T18518 T18518 C;Species: Erinaceus e C;Date: 15-Oct-1999 #s C;Accession: T18518 R;Lawn, R.M.; Boonmark A;Title: The recurring A;Reference number: I4 A;Accession: T18518 A;Status: preliminary; A;Molecule type: mRNA A;Roross-references: UN A;Experimental source: C;Comment: The lipoproent apolipoprotein(a).	Db 158 YCR Qy 205 DHQ Qy 205 TDV Qy 265 TDV Qy 265 TDV Qy 323 CRN Db 331 CRN Qy 366 KNY Qy 366 KNY Qy 360 QSY Qy 423 TGN Qy 423 TGN
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### ALIGNMENTS

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914210; Q02935; Q13494; Q14519; Q8TCEZ; Q9BYL9; Q9BYM0; Q9UDU6; Q1-JAN-1990 (Rel. 13, Created)

01-JAUG-1991 (Rel. 19, Last sequence update)

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Name-HGF; Synonyms-HPTA;
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                                                              SEQUENCE FROM N.A.
TISSUE=Placenta;
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                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      163:967-973 (1989)
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                                                                                                                                                  DOI=10.1038/342440a0;
M., Seki T., Shimonis
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Sakiyama O.,
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                 from human hepatocyte
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Takahashi K.,
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REDEINES-27379999; pubMed=12853948; DOI=10.1038/nature01782;
WARDLINES-27379999; pubMed=12853948; DOI=10.1038/nature01782;
WARDLINES-27379999; pubMed=12853948; DOI=10.1038/nature01782;
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WARDLINES-2737999; pubMed=12853948; DOI=10.1038/nature01782;
WARDLINESON C., Palebaunty K.D., Mass J., Jaeger S., Walker R.,
WARDLINES C., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
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ini L., Weidner K.M.,
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Hishida T., Daik
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MEDLINE=22844761; PubMed=12963274; DOI=10.1016/S0165-2427(03)00118-1;

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                                                                    Vanue-vec. (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :0006508; P:proteolysis and peptidolysis; II
ro; IPR001359; HGF MSTI.
ro; IPR000001; Kringle.
ro; IPR003014; PAN.
ro; IPR003509; Pan.app.
ro; IPR003509; Pan.app.
ro; IPR001314; Peptidase_S1.
ro; IPR001314; Peptidase_S1A.
ro; IPR001314; Peptidase_SY8.
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                                                                                                                                                                                                                                                                              YRGNGKNYMGNLSKTRSGLTCSMWEKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                             YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYPHQHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTLDPDTPWEYCAIKMCAHSTMNDTDVPMETTECIQGQGEGYRGTINTIWNGVPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
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         (Bovine)
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                                                      factor
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93.1%;
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Last sequence that annoted
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Pred. No. 2.9e
19; Mismatches
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Query Match
Best Local S
Matches 414
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EMBL; AB110822; BAD02475.1; -.
HSSP; P00819; 1KIV.
GO: GO:0004263; F:chymotrypsin activity; IEA.
GO: GO:0004263; F:chymotrypsin activity; IEA.
GO: GO:0008233; F:peptidase activity; IEA.
GO: GO:000823; F:trypsin activity; IEA.
GO: GO:0006508; P:proteolysis and peptidolysis; InterPro; IPR001359; HGF MSTI.
InterPro; IPR001359; HGF MSTI.
InterPro; IPR003609; Pan app.
InterPro; IPR00154; Paptidase S1.
InterPro; IPR00154; Peptidase S1.
InterPro; IPR0010154; Feptidase S1.
InterPro; IPR0010154; Feptidase S1.
InterPro; IPR0010154; Feptidase S1.
InterPro; IPR0010154; Kringle: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00051; Kring1: 4.

Pfam; PF00089; Trypsin; 1.

Pfam; PF00089; Trypsin; 1.

PIRSF; PIRSF001152; HGF MST1; 1.

PRINTS; PR000722; CHYMOTRYPSIN.

PRINTS; PR00018; KRINGLE.

ProDom; PD000395; Kringle; 4.

SMART; SM00130; KR; 4

SMART; SM00473; PAN AP; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE 1; 4.

PROSITE; PS50070; KRINGLE 2; 4.

PROSITE; PS50070; KRINGLE 2; 4.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.
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NCBI_TaxID=9913;
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Mammalia; Eutheria;
                                                                                                                  361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
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CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                               YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                                                                 QYPHQHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC
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                                                                                                                                                                                                                                                                                                                                                           MTCNGESYRGPMDHTETGKI CQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC
                                                                      YRGNGKNYMGSLSKTRSGLTCSMWDKNMEDLHRHIFWEPDATKLNKNYCRNPDDDAHGPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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Pred. No. 8.
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E39D653B0A85F49B CRC64;
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3.2e-176;
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Matches
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MEROPS; S01.982; -.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0006508; F:trypsin activity; IEA.

GO; GO:001359; HGF MST1.

InterPro; IPR001359; HGF MST1.

InterPro; IPR00301; Kringle.

InterPro; IPR003014; PAN.

R InterPro; IPR00314; Pan.app.

R InterPro; IPR001254; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R InterPro; IPR00103; Pept Ser_Cys.
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                 InterPro; IPR001314; Peptidase_S1.
InterPro; IPR009003; Pept Ser_Cys
Pfam; PF00051; Kringle; 4.
Pfam; PF00024; PAN; 1.
Pfam; PF00024; PAN; 1.
Pfam; PF00029; Trypsin; 1.
PIRSF; PR00722; CHYMOTRYPSIN.
PRINTS; PR007152; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRODOM; PR00018; KRINGLE.
PRODOM; PR00018; KRINGLE.
PR00103; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00120; TRYP SPC; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS00070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50070; KRINGLE_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; AB046610; BAB21499.1; --
EMBL; AB08187; BAC10545.1; --
HSSP, P14210; 1GMN.
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Kobayashi Y., 1
Tsujimoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BH09;
Q9BH09;
01-JUN-2001
01-JUN-2001
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Submitted
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9685;
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 121
                                   90
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                                                                                                                                                                                                Similarity
                                 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                        QKKRRNTLHEFKKSAKTTLIKEDPLLKIKTKKMNTADQCANRCIRNKGLPFTCKAFVFDK
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                                                                                                                                                                                                                                                     Kringle; Protease; Serine 728 AA; 83067 MW; 8D7F4
                                                                                                                                                                                 Conservative
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17,
27,
r HGF.
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Last
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                                                                                                                                                                               Score 2452; DB
Pred. No. 1.6e-1
1; Mismatches
                                                                                                                                                                                                                                                     Serine protease.
8D7F4A333D1E190A
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                                                                                              SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Thymus;
STRAIN-C57BL/6J; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A630060C16 product:hepatocyte growth factor, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meth.
                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome t60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                       SEQUENCE FROM N. I
STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8C9G5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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Rodentia;
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOI=10.1038/35055500;
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based o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA collection.";
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; Murinae; Mus
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annotation
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RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.
RA Houda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hoyashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itch M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya I.
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (UUL-2001) to the EMBL/denBank/DDBJ databases.

DR EMBL; AK042121; BAC31175.1; -.

RH MSSP; P14210; 1GNN.
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Best Local
Matches 40
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MGD; MG1:96079; Hgf.

GG); GG:00008283; P:cell proliferation; IDA.

GG); GG:0000902; P:cellular morphogenesis; ID

InterPro; IPR011159; HGF MST1.

InterPro; IPR000001; Kringle.

InterPro; IPR003014; PAN.

InterPro; IPR00314; Paptidase_S1.

InterPro; IPR00314; Peptidase_S1A.

InterPro; IPR00101314; Peptidase_S1A.

InterPro; IPR00101314; Peptidase_S1A.

InterPro; IPR00101314; Peptidase_S1A.

InterPro; IPR00101314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0018; KRINGLE.
PRODOM; PD000395; Kringle; 4.
SMART; SM00110; KR; 4.
SMART; SM00110; KR; 4.
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; TRYP_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50948; PAN; 1.
PROSITE; PS50940; TRYPSIN_DOM; 1
HYGIOLBES; Kringle; Procease; Se; SEQUENCE 728 AA; 82990 MW; 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00051; Kringle; 4.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001152; HGF MST1;
                                                                                                                                                                                                                                                                                                  Match
                                      153
 181
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                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                                                                                                           ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                        WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                               WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                              SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP
                                                                                                                                                                                        QKKRRNTLHEFKKSAKTTLTKEDPLLK1KTKKVNSADECANRC1RNRGFTFTCKAFVFDK
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                               92.5%;
91.1%;
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Pred.
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8D5258DF3BCF3545 CRC64;
                                                                                                                                                                                                                                                               Mismatches
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No. 2.7e-172;
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Okazaki Y.,
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RESULT 6
HGF_MOUSE
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 Q08048; Q61662; Q64007; Q01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hepatcoyte growth factor precursor (Scatter f. (Hepatcopoeitin A).
                                                                                                                                                                       Biochim Biophys. Acta 1216:299-303(1993).

- PUNCTION: HGF is a potent mitogen for mature parenchymal hepatocyte cells, seems to be an hepatotrophic factor, and act growth factor for a broad spectrum of tissues and cell types.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94363381; PubMed=8081873;
Lee C.C., Kozak C.A., Yamada K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary fibroblast;
MEDLINE=94183257; PubMed=8135822;
Sasaki M., Nishio M., Sasaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGF MOUSE
 <del>:</del>
                            +
                                                                                                                                                                                                                                                               MEDLINE=94060105; PubMed=8241272; DOI=10.1016/0167-4781(93)90159-B; Liu Y., Michalopoulos G.K., Zarnegar R.;
                                                                                                                                                                                                                                                                                                                                                           Lee C.C., Kozak C.A., Yamada K.M.;
"Structure, genetic mapping, and expression of the mouse Hgf/scatter
fastor game ".
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki M., Nishio M., Sasaki T., Enami J.;
"Identification of mouse mammary fibroblast-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor as hepatocyte growth factor."
                                                                                                                                                                                                                                "Molecular cloning and characterization hepatocyte growth factor.";
                                                                                                                               growth factor for a broad spectrum of tissue has no detectable protease activity. SUBUNIT: Dimer of an alpha chain and a beta disulfide bond.
                            SIMILARITY:
subfamily.
SIMILARITY:
                                                           Name=Short;
                                                                                                 Event=Alternative
                                                                                                                   ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                    Adhes. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213
                                                                       IsoId=Q08048-1;
                                          IsoId=Q08048-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTGNPLIPWDYCPISRCEGDTTPTIV 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTGNPLIPWDYCPISRCEGDTTPTIV 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTLDPDTTWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHI FWEPDASKLNKNYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
Contains 4 kringle domains
                            Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Res. Commun. 199:772-779(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORMS
                                                                                                                                                                                                                                                                                                                                       1:101-111(1993).
                           Sequence=VSP_005408;
gs to the peptidase S
                                                                     Sequence=Displayed;
                                                                                                  splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                    Named isoforms=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND SHORT),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                               of cDNA encoding mouse
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                            family.
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                                                                                                                                                chain
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                            Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammary
                                                                                                                                             linked by
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Query Match
Best Local S
Matches 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00051; Kringle; 4.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; Trypsin; 1.
Pfam; PF00089; Trypsin; 1.
PRSF; PIRSF001152; HGF MST1; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR000135; KRINGLE.
PRODOm; PD000395; Kringle; 4.
                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00130; KR; 4.

SMART; SM00473; PAN AP; 1.

SMART; SM00020; TXYP SPC; 1.

PROSITE; PS00021; KRINGLE 1; 4.

PROSITE; PS50070; KRINGLE 2; 4.

PROSITE; PS50048; PAN; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                               CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                        DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D10212; BAA01064.1; -.
EMBL; D10213; BAA01065.1; -.
EMBL; S71816; AAB31855.1; -.
EMBL; X72307; CAA551054.1; ALT_INIT.
PIR; JC2117; A60185.
HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003609; Pan app.
InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                         Alternative splicing; Direct protein sequencing; Glyo
Growth factor; Kringle; Pyrrolidone carboxylic acid;
Serine protease homolog; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:96079; Hgf.
GO; GO:0008283; P:cell proliferation;
GO; GO:0000902; P:cellular morphogene
                                                                                                           VARSPLIC
                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS;

    !- SIMILARITY: Contains 1 PAN domain.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S01.982;
             Similarity
                                                                                                           129
212
212
306
396
396
396
496
496
295
295
569
6569
  Conservative
                                                 Ā
                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN_DOM; 1.
                                                                                                           124
207
289
384
470
728
97
728
607
295
569
569
                                               82944 MW;
             92.5%;
91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        morphogenesis; IDA.
  21;
                                                           Missing (in isoform & /FTIG=VSP 005408.
N -> K (in Ref. 2).
V -> L (in Ref. 2).
R -> H (in Ref. 3).
 Score 2408; DI
Pred. No. 3.2e
21; Mismatches
                                                                                                                                                                                                                                Kringle 1.
Kringle 2.
Kringle 3.
                                                                                                                     Interchain (By similarity).

N-linked (GlCNAC. . ) (Pot
                                                                                                                                                                                Serine protease-like.
By similarity.
By similarity.
                                                                                                                                                                                                                     Kringle 4
                                                                                                                                                                                                                                                                      PAN
                                                                                                                                                                                                                                                                                             Pyrrolidone carboxylic
                                                                                                                                                                                                                                                                                                      Hepatocyte growth factor alpha chain. Hepatocyte growth factor beta chain.
                                                                                                                                                                                                                                                                                                                                By similarity.
                                               -> L (in Ref. 2).
-> H (in Ref. 3).
A0381FC497534328 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
            DB 1;
.2e-172;
                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
cid; Repeat;
                         Length
                                                                                                            Short).
   Indels
                                                                                                                                (Potential). (Potential). (Potential).
                                                                                                                       (Potential)
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  Gaps
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collaboration - L outstation -

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RESULT 7
                            MEDINE=91031482; PubMed=2146117;

MEDINE=91031482; PubMed=2146117;

A Okajima A., Miyazawa K., Kitamura N.;

"Primary structure of rat hepatocyte growth factor and inductio
"Primary structure of rat hepatocyte growth factor and inductio
"Eur. J. Biochem. 193:375-381(1990).
-!- FUNCTION: HGF is a potent mitogen for mature parenchymal
hepatocyte cells, seems to be an hepatotrophic factor, and average and description of tissues and cell types.
-!- SUBUNIT: Dimer of an alpha chain and a beta chain linked hy a
subfamily Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGF_RAT
P17945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hepatocyte growth factor precursor (Scatter f. Hepatopoeitin A).
                                                                                                                                                                                                                                                                                                             "Deduced primary structure of rat hepatocyte groexpression of the mRNA in rat tissues.";
Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990)
                                                                                                                                                                                                                                                                                                                                                             Toshiro K., Hagiya M., N
Shimizu S., Nakamura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Wistar; TISSUE=Liver; MEDLINE=90222197; PubMed=2139229;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Hgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
subfamily.
SIMILARITY: (SIMILARITY: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTLDPDTPWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHI FWEPDASKLNKNYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
 Contains
                   Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL
 kringle
PAN doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                               Seki T.,
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                                                                                                                                                                                                                                                                                                                                                                               Shimonishi
                                                                                    chain linked by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Murinae; Rattus.
                                                  Plasminoger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SF
                                                                                                                                                                                        nd induction injury.";
                                                                                                                      types.
                                                                                                                                        acts
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Best Local S
Matches 404
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PIRSF; PIRSF001152; HGF MST1; 1
PRINTS; PR00712; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PrODOM; PD000395; KRINGLE; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00473; PAN_AP; 1.
PROSITE; PS00070; KRINGLE_1; 4.
PROSITE; PS00070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
                                                                                                                                                                                                                                                                                                         DOMAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X54400,
PIR; A35644; A35644.
PIR; D14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct protein
Pyrrolidone car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00051; Kringle; Pfam; PF00024; PAN; 1. Pfam; PF00089; Trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
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EMBL; X54400;
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c; IPR003014; PAN.
c; IPR003060; Pan app.
c; IPR009003; Pept Ser Cys.
c; IPR001254; Peptidase S1.
c; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S01.978; -.
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50948; PAN; 1.

PS50240; TRYPSIN_DOM; 1.
                    WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                           SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP
                                                                                               ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                                                      QKKRRNTLHEFKKSAKTTLTKEDPLVKIKTKKVNSADECANRCIRNKGFPFTCKAFVFDK
                                                                                                                                                                               ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                                                                                                                                                                                                                                             728
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                                                                                                                                                                                                                                                  92.2%;
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                                                                                                                                                                                                                                                                                                  ringle 1.

Kringle 2.

Kringle 3.

Kringle 3.

Kringle 4.

Serine protease-like.

By similarity.

By similarity.

Interchain (By similarity).

Interchain (GlcNAC. . .) (Poten N-linked (GlcNAC. . .) (Poter N-linked (GlcNAC. . .)) (Poter N-linked (GlcNAC. . .) (Poter N-linked (GlcNAC. . .)) (Poter 
                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                               Score 2401; DB 1;
Pred. No. 1.1e-171;
3; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrrolidone carboxylic similarity).
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Hepatocyte growth factor beta chain.
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                                                                         Query Match
Best Local S
Matches 341
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HSSP; P14210; TGMN.

GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:cpeptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysi
Pfam; pF00051; Kringle; 4.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001152; HGF MST1; 1.
                                                                                                                                                                                                          PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0018; KRINGLE.
PRODOM; PD000395; KRINGLE.
PRODOM; PD000395; KRINGLE; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; TRYP; SPC; 1.
SMART; SM00020; TRYP; SPC; 1.
PROSITE; PS00021; KRINGLE; 4.
PROSITE; PS50070; KRINGLE; 4.
PROSITE; PS50948; PAN; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
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Q90978; Q90866;
01-JAN-1998 (TYEMBLrel. 05, Cree
01-JAN-1998 (TYEMBLrel. 26, Last
01-MAR-2004 (TYEMBLREL. 26, Last
Hepatocyte growth factor /scattt
Name=HGF/SF;
Gallus (Chicken).
Ebkaryota; Metazoa; Chordata; Cr
                                                                                                                                                              SMART; SM00
PROSITE; PS
PROSITE; PS
PROSITE; PS
PROSITE; PS
PROSITE; PS
Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96029010; PubMed=7554499; Thery C., Sharpe M.J., Batley S.J., "Expression of HGF/SF, HGF1/MSP and during early chick development."; Dev. Genet. 17:90-101(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to peptidase EMBL; X84045; CAA58864.1; -. PIR; I51285; I51285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria; Aves;
                                                                         Local Similarity
les 341; Conserv
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                          KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR
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  726
                                                                                                                                                                                         Kringle;
                                                                           Conservative
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                                                                                                                                                                 Protease; Serine
82865 MW; 5BD060
                                                                                               78.8%;
76.6%;
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26, Last annotation update)
/scatter factor.
                                                                      49;
                                                                      Score 2052; DE
Pred. No. 1.6e-
49; Mismatches
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; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                 Serine protease.
5BD06CFB5C40B003 CRC64;
  peptidolysis;
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c-met
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                                                                      DB 2;
.6e-145;
les 53;
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                                                                         Gaps
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                                                                                                                                                                                    MEROPS; S01.976; -...

GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:00008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidol
pfam; PF00051; Kringle; 4.
pfam; PF00089; Trypsin; 1.
pfam; PF00089; Trypsin; 1.
pfixe; PFRSF001152; HGF_MST1; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRODOM; PD000395; KRING1e; 4.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN AP; 1.
SMART; SM000473; PAN AP; 1.
PROSITE; PS00021; KRINGLE 1; 4.
PROSITE; PS50070; KRINGLE 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91402;
Q91402;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura H., Tashiro K., Nakamura T., "Molecular cloning of Xenopus HGF cDN Xenopus early embryogenesis.";
Mech. Dev. 49:123-131(1995).

Nech. Belongs to peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2004 (TrEMBLrel. 2
Hepatocyte growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatocyte
Name=HGF;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S77422; AAB34354.2;
HSSP; P14210; 1GMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Tailbud;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus
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iro K., Nakamura
ig of Xenopus HGF
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                                                                                                                                                                                                                                                                                         peptidolysis;
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Best Local S
Matches 305
           MEDLINE=95237013; PubMed=7720585;
Streit A., Stern C.D., Thery C., Ireland G.W., Ap.
Streit A., Stern C.D., Thery C., Ireland G.W., Ap.
Sharpe M.J., Gherardi E.;
"A role for HGF/SF in neural induction and its ex
node during gastrulation.";
Development 121:813-824(1995).
EMBL; X80131; CAA56430.1; -
HSSP; P00747; IKIO.
InterPro; IPR003001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003509; Pan_app.
Pfam; PF00051; Kringle; 4.
Pfam; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                    Q788Q2
Q788Q2;
Q788Q2;
05-JUL-2004
05-JUL-2004
HGF/SF prote
                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50948; PAN; 1.
PROSITE; PS50940; TRYPSIN_DOM;
Hydrolase; Kringle; Protease; 1.
SEQUENCE 710 AA; 81487 MW;
                                                                                                                                                                                                                                                            HGF/SF protein
Name=HGF/SF;
                                                                                                                                                                SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                                                                                 NCBI_TaxID=9031;
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  PR00018;
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Pred. No. 1.8e:
64; Mismatches
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; Galliformes; Phasianidae; Phasianinae;
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5FE6480BE31C27FC CRC64;
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No. 1.8e-131;
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SMART; SM00130; KR; 3
SMART; SM00473; PAN A
PRÖSITE; PS00021; KRI
PROSITE; PS50070; KRI
PROSITE; PS50948; PAN
Kringle; Signal;
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LOC397993 protein.
Name=LOC397993;
Nemopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6GP14;
Q6GP14;
05-JUL-2004
05-JUL-2004
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MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D. Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S., Bosak S.A., McEwann K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=Spleen;
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PS00021; KRINGLE 1;
PS50070; KRINGLE 2;
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Signal.
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Best Local :
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ dat

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ dat

EMBL; BC07334; AAH73334.1; -.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:000599; F:thrombin activity; IEA.

GO; GO:0007596; P:blood coagulation; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis;

InterPro; IPR000001; Kringle.

InterPro; IPR003014; PAN.

InterPro; IPR003014; PAN.

InterPro; IPR003016; Pan app.

InterPro; IPR003016; Paptidase_S1A_pr.

Pfam; PP00051; Kringle; 4.

Pfam; PP00054; PAN; 1.
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SMART; SM00130; RAN AP; 1.

PROSITE; PS00021; KRINGLE 1; 4

PROSITE; PS50070; KRINGLE 2; 4

PROSITE; PS50948; PAN; 1.
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SEQUENCE
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
PRODOm; PD000395; Kringle; 4.
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SHRFLPEKYPCKGLDENYCRNPDGSEAPWCFTTLPGMRMAYCFQIKRCKDDVLEPDCYHG
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r L., Pontius J., Clifto
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RESULT 12
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Best Local S
Matches 207
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SMART; SM00130; KR; 4.

SMART; SM00473; PAN Ap; 1.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS00021; KRINGLE 1; 4.

PROSITE; PS50070; KRINGLE 2; 4.

PROSITE; PS500748; PAN; 1.

PROSITE; PS500748; PAN; 1.

PROSITE; PS500740; TRYPSIN DOM; 1.

PROSITE; PS500740; TRYPSIN DOM; 1.
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01-NOV-1996
01-NOV-1996
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Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Phasianidae; Phasiani
אייר ארים אומים אומי
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GG; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1994 (TrEMBLrel. 26, Last annotation update)
Hepatocyte growth factor-like/macrophage stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00051; Kringle; 4.
pfam; PF00024; PAN; 1.
pfam; PF000089; Trypsin; 1.
process; Pirsf001152; HGF_MST1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X84043; CAA58862.1; -. HSSP; P00747; ICEA.
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207; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR00018; KRINGLE
                                                                                                           IPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCN
                                                                                                                                                                                                                                                              CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM
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       GESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLD
                                                                              TPHDHRFLPSLRNG--
                                                                                                                                                                                                                CQLLPWSQRSPGARLQKNIHYDLYQKKDFLRECIVANGTSYRGTRDTTERGLRCQHWQAT 135
                                                                                                                                                                                                                                                                                                                                                    RSPLNDFQRLRGTELRAAPNEPPPSAPAHGAAQQCAQRCANRP----DCRAFHHERQSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.4%;
                                                                       LEENYCRNPDRDKRGPWCYTVDPNVRHQSCGIKKCEDAVCMTCN
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Pred. No. 2.4e-82;
1; Mismatches 149
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Best Local S
Matches 207
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SMART; SM00473; PAN AP; 1.

SMART; SM00020; Tryp SPc; 1.

PROSITE; PS00021; KRINGLE 1; 4.

PROSITE; PS50070; KRINGLE 2; 4.

PROSITE; PS50948; PAN; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00024; PAN; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001152; HGF MST1; 1.
PRINTS; PR00725; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; Kringle; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
HSSP;
GO; GC
                                                                                                                                                                                                                                                                 Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Growth factor Livertine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruiz i Altaba A., Thery C.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMBL; U57455; AAB52574.1; -.
ISSSP; P00746; IFDP.
ISSSP; GO:0005509; F:calcium ion binding; IEA.
IO; GO:0004263; F:chymotrypsin activity; IEA.
IO; GO:0008233; F:peptidase activity; IEA.
IO; GO:0008239; F:thrombin activity; IEA.
IO; GO:0004295; F:trypsin activity; IEA.
IO; GO:0007596; P:blood coagulation; IEA.
ID; GO:0006508; P:proteolysis and peptidolysis;
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        65
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                                                      31
                                                                                                          <sub>5</sub>
                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHI-----FWEPDASKLNENYCRNPDDDDAH
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     CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM
                                                                                                     RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĠPŴĊŸTMDPRTPFĎŸĊAÍKPĊSĠSAVPSVL
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                                                                                                                                                                                                                                                                 Kringle;
716 AA;
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                              Protease;
81971 MW;
                                                                                                                                                                               46.48;
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01,
26,
                                                                                                                                                         Score 1208; DE Pred. No. 3.2e-75; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                 Serine protease.
508376A0E4398798
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                                                                                                                                                         ; DB 2;
3.2e-82;
hes 149;
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ia; Pipoidea; Pipidae;
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                                                                                                                                                         Skeel A.,
Leonard E.
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P26927; Q13350; Q14870;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hepatocyte growth factor-like protein precursor (Mastimulatory protein) (MSP) (Macrophage stimulating Name=MST1; Synonyms=HGFL;
                                                                            "Macrophage stimulating protein: sequence, and cellular activity.' J. Exp. Med. 173:1227-1234(1991)
                                                                                                                                                                                                                                                                                                                                MEDLINE=93340141; PubMed=8393443; Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.; Yuhki N., Wang M.H., Skeel A., Leonard E.J.; Political Properties and expression of human macrophage stimulating protein (MSP, MST1) confirms MSP as a member of the family of kringle proteins and locates the MSP gene on chromosome 3."; J. Biol. Chem. 268:15461-15468(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the DNF152 locus on identification of a gene coding for four to hepatocyte growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92002016; PubMed=1655021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                             PubMed=1827141;
                                                                                                                                                                                                                                   TISSUE=Plasma;
                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                        FÜNCTION: Probably has no proteolytic activity, characteristic of serine proteases catalytic si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440
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                                                                                                                                                                                                                                                           OF 230-247;
AND SUBUNIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e growth factor.";
30:9768-9780(1991).
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                                                                                                                                                                                                                                                                                       288-310; 326-341;
                                                                                                                                                                                    Showalter
                                                                                                                             purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus on human chromosome
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InterPro; IPRO00001; Kringle.
InterPro; IPRO03004; PAN.
InterPro; IPRO03609; Pan app.
InterPro; IPRO03609; Pan app.
InterPro; IPRO03003; Pept Ser Cys.
InterPro; IPRO0303; Pept Ser Cys.
InterPro; IPRO0314; Peptidase S1.
InterPro; IPRO0314; Peptidase S1A.
InterPro; IPRO0316; Peptidase S1A.
InterPro; IPRO0316; Peptidase S1A.
InterPro; IPRO0316; Peptidase S1A.
InterPro; IPRO0316; Rringle; 4.
Pfam; PF000024; PAN; 1.
Pfam; PF000084; Trypsin; 1.
Pfam; PF000084; Trypsin; 1.
PRINTS; PR0001152; HGF MST1; 1.
PRINTS; PR001152; HGF MST1; 1.
PRINTS; PR001152; PROTHROWBIN.
PRODOM; PR000395; Kringle; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; Tryp Spc; 1.
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PROSITE;
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Genew; HGNC:7380; MST1
MIM; 142408; -...
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EMBL; U37055; AAC50471.1; -.
EMBL; L11924; AAA59872.1; -.
EMBL; A40331; A47136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subfamily.
SIMILARITY: Contains
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                                                                                                                                                                                                                                                                                                                                                                                            SM00130; KR; 4.

SM00473; PAN AP; 1.

SM00020; Tryp_SPc; 1.

SM00020; KRINGLE 1; 4.

E; PS50070; KRINGLE 2; 4.

E; PS50948; PAN; 1.

E; PS50240; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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Kringle 3.
Kringle 4.
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Serine protease-like.
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Best Local S
Matches 197
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CARBOHYD
                                                                                                                                                    P70006; PRELIMINARY; PRT; 7970006; PRELIMINARY; 7970006; O1-FEB-1997 (TrEMBLrel. 02, Last seque 01-FEB-1997 (TrEMBLrel. 26, Last annot 1-MAR-2004 (TrEMBLrel. 26, Last annot Hepatocyte growth factor-like protein xenopus laevis (African clawed frog).
              SEQUENCE FROM N.A.
TISSUE-Kidney, and Liver;
MEDLINE=96404125; PubMed=8808403;
Abberger F., Schmidt G., Richter K.
                                                                                                                       Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; M
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                                                                                       Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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 Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                              WCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCFRGKGEGYRGTANTTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDGSEAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECQRWDLQHPHQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVRTCIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEENFCRNPDGD
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   hepatocyte
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E -> K (in dbsNP:7798)

/FTId=VAR 014569.

R -> G (in Ref. 3).

C -> E (in Ref. 3).

R -> E (in Ref. 3).

PS -> SL (in Ref. 3).

PS -> E (in Ref. 3).

V -> E (in Ref. 3).
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N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
Y->C.
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Last annotation updat
                                                                                                                         Mesobatrachia;
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C -> F
                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
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                               DOI=10.1016/0925-4773 (95) 00458-0;
 growth
                                                                                                                                                                                                                                                  717
                                                                                                                                                                    precursor.
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                                                                                                                         Pipoidea; Pipidae;
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T specifically expressed in the presumptive neural plate of gastrulation.";

If Mech. Dev. 54:23-37(1996).

Rembl. 708734; CAA69999.1; -.

Rego; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:000523; F:calcium ion binding; IEA.

Rego; GO:0004263; F:chymotrypsin activity; IEA.

Rego; GO:0008203; F:chymotrypsin activity; IEA.

Rego; GO:0003809; F:chymobin activity; IEA.

Rego; GO:0004295; F:trypsin activity; IEA.

Rego; GO:0003809; F:thrypsin activity; IEA.

Rego; GO:0004295; F:trypsin activity; IEA.

Re
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Best Local Similarity
Matches 201; Conserv
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SMART; SM00473; PAN AP; 1.

SMART; SM00020; TYPP SPC; 1.

PROSITE; PS00021; KRINGLE 1; 4.

PROSITE; PS50040; TRYPSIN_DOM; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00051; Kringle; 4.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001152; HGF MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
PRODOm; PD000395; Kringle; 4.
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                                              NGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYT
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                                                                                                                                                                                                                                                                                                                                                                                       GEDYRGSVDRTESGKECQRWDLQAPHTHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSALNDYORSKGLELVHMNEG-GVKOEVQAEIQICAKQCSD----LLDCRSFDYNWKSQS
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NGELYRGRVSKTRKGIMCRRWEEKQNDLELSLA-QPYLVPLEENYCRNPDRDSHGPWCYT
                                                                                                                               VHRFLPEKYPCKGLDENYCRNPVGSEAPWCFTTLKNMRMAYCFQIKRCTDDVVEPECYHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 717 hepatocyte growth factor-like protein. 717 AA; 82017 MW; 6F877A432CBCDD54 CRC64;
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; Pred. No. 8.1e-80;
78; Mismatches 152;
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Search completed: October Job time : 69.3656 secs

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Gapop 10.0 , Gapext 0.5
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2604
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first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	ທ	4	ω	N		No.	Result
2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	2601	Score	
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Human		Hepato	Human	Aaw39207 Human hep		Aaw58696 Human hep	Aaw59922 Human leu	Aaw00338 Human hep	Aaw00340 Wild type	Aar87523 Mutant he	Aar87525 Mutant he	Aar87524 Mutant he	Aar87522 Mutant he	Aar42062 Vascular	Aar40863 Competati	Aar40862 Competati	Aar20005 Human hep	Aar25676 Recombina	Aau04275 Nuclear l	Aab45838 Nucleic a		Aay98485 Hepatocyt	Human	37393 Human h	Description	

Query Match

99 .98;

Score

2601;

DB 7;

Length

447;

Sequence 447 AA;

Human hep	Aar52943	AAR52943	2	728	98.5	2565	5
Human hep	Aar52940	AAR52940	2	728	98.5	2565	44
Human hep	Aar52948	AAR52948	2	728	98.5	2565	3
Human hep	Aar52944	AAR52944	N	728	98.5	2565	42
Human hep	Aar52947	AAR52947	N	728	98.5	2565	41
Human hep	Aar52945	AAR52945	2	728	98.5	2565	40
Human hep	Aar52942	AAR52942	2	728	98.5	2565	39
Human hep	Aar52941	AAR52941	2	728	98.5	2565	38
Human hep	Aar12792	AAR12792	N	728	98.5	2565	37
Hepatocyt	Aar47227	AAR47227	N	728	99.0	2577	36
Human hep	Aaw88530	AAW88530	N	728	99.3	2586	35
Human hep	Aaw88531	AAW88531	N	728	99.3	2587	34
Human hep	Aaw88532	AAW88532	N	728	99.4	2588	33
Human hep	Aaw88529	AAW88529	N	728	99.5	2591	32
Hepatocyt	Aar39521	AAR39521	N	728	99.7	2595	31
Human hep	Aar14243	AAR14243	N	728	99.7	2595	30
Human leu	Aar15623	AAR15623	2	728	99.7	2595	29
Hepatic p	Aar10656	AAR10656	N	727	S	2595	28
N-termina	Aay57173	AAY57173	ω	447	ū	2599	27
Cnimeric	Ads19044	ADS19044	α	75E	99.9	2601	26

## ALIGNMENTS

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RESULT 1
ADE37393
ID ADE3
The invention comprises a conjugate that contains an N-terminal fragment of hepatocyte growth factor (HGF/SF) consisting of the hairpin domain and the four kringle regions of the alpha-chain and 1-3 polyethylene glycol (PEG) groups. The conjugate of the invention is useful for the preparation of a medicament for the treatment of cancer. The present amino acid sequence represents the human N-terminal four kringlecontaining fragment of hepatocyte growth factor (NK4).
                                                                                                                                                                        Conjugate comprises an N-terminal fragment of hepatocyte growth factor consisting of the hairpin domain and the four kringle regions of the alpha-chain and one to three polyethylene glycol groups, useful for treating cancer.
                                                                                                                                                                                                                                                    WPI; 2003-749561/71.
N-PSDB; ADE37392.
                                                                                                                                              Disclosure; SEQ ID NO 2; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                        23-FEB-2001; 2001EP-00104640
                                                                                                                                                                                                                                                                                                                                                                                                                     EP1234583-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human hepatocyte growth factor N-terminal four kringle fragment.
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                                           New NK14
                                                                                WPI; 2003-897946/82
N-PSDB; ADM83264.
                                                                                                                                           Nakamura
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(MATS/)
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Best Local Similarity
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  20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                     carcinogenesis;
                                                                                                                                                                                                                                          Transporter system; nucleic acid delivery; gene therapy;
                                                                                                                                                                                                                                                                                                                      31-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                      (first entry)
  92US-00855389
93WO-US002725
                                                             93US-00167641
                                                                                                                                                                                                                       cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                    697
                                                                                                                                                                                                                                                                               20 used in nucleic acid transporter system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a transporter system for delivering concleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for transporting nucleic acid into cells, useful e.g. in gene y and for generating transgenic animals, comprises binding agent to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                                                                                                                                                      QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                                                                                                                                                                                                                                                                                                                                         MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                                                                                     CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                                     YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEFDASKLNENYCRNFDDDAHGFW
                                                                                                                                                                                                                 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                                                                                                                                                                                                                                                                   YTLDPHTRWEYCAIKTCADNTWNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARKQCLWFPFNSMSSGVKKBFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                                                                                                                                                                                  YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                     WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                  CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                    YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHI FWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          without requiring
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                                                                                                                                                                                                                                                                                                                                                  YRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
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Pred. No. 8.7e-165;
1; Mismatches 0;
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AAY59030 standard;

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                                                                                                                                                                                                                                                                  cc delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components; (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or cc antigen or is capable of entering a cell through cytosis; (c) a nucleic cc acid or macromolecular molecule binding moiety; (d) a moiety that is cc capable of moving or initiating movement through a nuclear membrane; and/ cor (e) a lysis moiety that enables the transport of the entire complex cc from the cell surface directly into the cytoplasm of the cell. The NTS conditions of the cell as the nucleus cof specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create ctransgenic animals for assessing human disease, such as cancer, in an cc animal model. The NTS can be used in vitro with tissue culture cells. The Specific expression into specifically targeted tissue culture cells. The Cc specific expression into specifically targeted tissue culture cells. The Cc decradation
                                                                                                                                                                                                       Query Match
Best Local S
Matches 446
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19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                 Sequence 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assessing human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOO SLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a nucleic acid transport system (NTS) vering nucleic acid into a cell. The NTS contains but is no
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                                                                                                                                                                 1 ERKRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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                                                                                                                                                                                                                      Similarity
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                                               WSSMI PHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDI PQCSEVEC
MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                            WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                        ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRS:
                                                                                                    ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                                               QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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93WO-US002725.
93US-00167641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease
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Pred. No. 8.7e-
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sparrow
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3.7e-165;
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                                                                                                                                                                                                                                  Length
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l model.
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20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
          acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, applipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of antigens.
                                                                                                                                               This invention describes a novel system (1) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic nuclear ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid delivery; nucleic acid transporter growth factor; clotting factor; apolipoprotein; tumor antigen; tumor suppressor; viral antigen;
                                                                                                                                                                                                                                                                     Claim 8;
                                                                                                                                                                                                                                                                                                     growth factors, enzymes, hormones,
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                        Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid transporter system peptide ligand SEQ ID
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   endosomal/lysosomal
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                                                                                                                                                                                                                                                                                                   c acid transporter system for delivering nucleic acid for delivering proteins and polypeptides to cells, in factors, enzymes, hormones, and tumor suppressors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTGNPLIPWDYCPISRCEGDTTPTIV 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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                                                                                                                                                                                                                                                                     Col 115-118; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                        Sparrow
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93WO-US002725.
93US-00167641.
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   degradation seen with prior art
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receptor; drug; oncogene;
parasitic antigen;
   systems
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Matches 446; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                           20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                       gene therapy;
                                                                                                                                                                                                                                   Nucleic acid
                                                                                                                                                                                                                                                       Nuclear ligand Pep20 used in nucleic acid transporter
                                                                                                                                                                                                                                                                             23-OCT-2001
                                                                                                                                                                                                                                                                                                                    AAU04275
                             WPI; 2001-365933/38
                                                                                                                                      05-JUN-1995;
                                                                                                                                                           23-JAN-2001
                                                                                                                                                                               US6177554-B1
                                                                       (BAYU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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                                                                                                                                                                                                                                                                                                                    standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑĀ,
                                                                                                                                                                                                                                   transport; cytosis;
                                                                                                                                                                                                                                                                            (first entry
                                                                                                                                                                                                                        hepatocyte;
                                                                                           92US-00855389.
93WO-US002725.
93US-00167641.
                                                                       COLLEGE MEDICINE
                                                                                                                                       95US-00462040
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                                                    Cristiano
                                                                                                                                                                                                                          muscle;
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Pred. No. 8.7e-165;
                                                   RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                        ligand; lysis; bone forming
                                                    Gottchalk
                                                                                                                                                                                                                                                                                                                                                                                              447
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                                                   ω
                                                                                                                                                                                                                          agent;
cell.
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                                                   Sparrow
                                                                                                                                                                                                                                                         system
                                                                                                                                                                                                                                   spacer molecule;
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Nucleic acid transport system, useful

system, useful for such as cancer in

creating transgenic animals for an animal model.

assessing human disease

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ARZSGAT
ID AARZS
XX AARZ
XX AARZ
XX AARZ
XX Reco
XX HGF;
XW Clin
XX Clin
XX HGF;
XW JP04
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PN JP04
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Best Local
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                                                                                                                                                                                                                                                                                      Recombinant human hepatocyte growth factor
19-NOV-1990;
                                                    30-JUN-1992
                                                                                                       JP04183394-A
                                                                                                                                                                                                              clinical diagnostic
                                                                                                                                                                                                                                                                                                                                                 20-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                      AAR25676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR25676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                           enhance growth; preparing transgenic animals; hepatic
ical diagnostic reagent; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
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90JP-00314548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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Pred. No. 8.7e-165;
1; Mismatches 0;
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RESULT 8
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AAC AAR2
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DE Huma
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KW HGF;
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KW HGF;
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HOMC
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HOMC
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PN EP46

Human hepatocyte 24-MAR-1992 AAR20005;

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entry

AAR20005 standard;

protein;

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Homo sapiens

HGF; kidney regeneration; nephritis

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Matches 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 728
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No. 9.1e-165;
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RESULT 9
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Best Local Simi
Matches 446;
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N-PSDB;
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                            AAR40862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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DB; AAQ20049.
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Matches 446
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                         MTCNGESYRGIMDHTESGKICQRWDHQT¤HRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                                                                                                                                                                                           WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                                                                                                                                                                            ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                                                                                                                                                                                              QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                                                                                                                                                                                                                                               ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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                                                         QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                                                                         YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                            MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                                                                                                                                                                              WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                                                                                                                                                               ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
               YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                          QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                                                         YTLDPHTRWEYCAI
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nilarity 99.8%;
Conservative
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32. .728
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                                                                                                                                                                                                                                                                                                                                               Score 2601; DB 2;
Pred. No. 9.1e-165;
1; Mismatches 0;
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hepatocyte

growth

Length

0

Gaps

0

91

RGTVNTIWNGIPCORWDS

331 300 271

420 391 360 240

180 151 120

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RESULT 10
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ID AAR40
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                                                                                                                                                                                           Query Match
Best Local Simi
Matches 446;
                                                                                                                                                                                                                                                               Sequence 728 AA;
                                                                                                                                                                                                                                                                                                              The gene encodes an inhibitor of HGF, which has a molecular weight of ca. 76000 to 92000 as determined by SDS-PAGE. Human modified (NP) HGF-A and -B fragments were prepared from human HGF CDNA. This was amplified by PCR to give a human NP-HGF DNA fragment that was transformed into E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein is competitive inhibitor of in animal model of liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-DEC-1991;
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                                                                                                                                                                                                           Similarity
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                                                                                                                                          ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                                                                                                                                                                                                                                                                                                                                   Page 11-14; 20pp; Japanese.
                   WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                         ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                        QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTGNPLIPWDYCPISRCEGDTTPTIV 478
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                                                      ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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Conservative
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9.1e-165;
nes 0;
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                                                                                                                                                                                                                          Length 728;
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 Query Match
Best Local Similarity
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RESULT 11
AAR42062
                                                          Sequence
                                                                                                  This sequence represents a single chain protein which selectively enhances the growth of vascular endothelial cells. This protein was produced by the human tumour cell line HUCCA-II or HUCCA-III. This protein enhances the formation of new blood vessels and may be used to enhance healing of wounds, burns injuries, decubitus or post-operative tissue damage. It may also be used as a drug for cardiac angiopathy. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                          Vascular endothelial cell growth factor protein - used for promoting angiogenesis in the treatment of cardiac angiopathy, wounds, burn injuries, postoperative tissue damage etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhance; growth; vascular endothelial cell; human; tumour; c HUOCA-II; HUOCA-III; blood vessel; wounds; burns; decubitus; post-operative tissue damage; drug; cardiac angiopathy.
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1992;
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15-NOV-1993
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DB; AAQ45702.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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                                  Disclosure; Page; 8pp; Japanese
                                                                   Novel derivative of hepatocyte growth factor positions 492-494, for use in treating injured
                                                                                                                            WPI; 1996-035890/04.
                                                                                                                                                                                              07-MAY-1994;
                                                                                                                                                                                                                                 07-MAY-1994;
                                                                                                                                                                                                                                                                                                      JP07304796-A
                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 491. .495
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   the
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   hepatocyte
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                                                                       comprises a mutation blood vessels.
     (HGF)
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 RESULT 13
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ID AAR877524
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AC AAR87
XX 21-JU
DT 21-JU
DT 21-JU
DX Mutar
XX Hepat
KW injuu
XX Syntl
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Best Local S
Matches 446
                                                                                                                                                                            Hepatocyte growth factor; protease; cleavage recognition injury; blood vessel; point mutation.
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                    JP07304796-A
                                                                                       Key
Misc-difference
                                                                                                                                           Synthetic
                                                                                                                                                                                                                                 Mutant hepatocyte growth factor #3 with changes at residues 491-495.
                                                                                                                                                                                                                                                                                                                                         AAR87524
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446; Conserv
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llarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                     (first entry)
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       protein;
                                                      te= "change from wild type
to Lys-Gln-Gly-Arg-Thr"
                                                                                    . 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2601; DB 2;
Pred. No. 9.1e-165;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 478
                                                                       sequence: Lys-Glu-Leu-Arg-
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amino acid changes at residues 492-494. (Note - this sequence is not given in the specification but is based on the HGF sequence given in AAR20005). The generated mutant contains the sequence Ile-Glu-Gly-Arg-Thr, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF is translated as single chain protein which is activated to a two chain protein by protease cleavage between residues 494-5, producing the alpha and beta chains. The novel sequence alters the protease recognition site, putatively introducing a Factor Xa recognition site. The novel HGF deriv. can be activated specifically at the site of injury in a blood vessel. (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were generated by point mutations using the oligonucleotides AAT06762-5

Length 728; Indels 0 Gaps

91

ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDY1RNC11GKGRSYKGTVS1TKSGIKCQP ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120 151

WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180 211

MTCNGESYRGLMDHTESGKI CQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 300 271

OXPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPN1RVGYCSQ1PNCDMSHGQDC YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS

QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC

451 420 391 360 331

site; Factor Xa;

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RESULT 14
AAR87525
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AC AAR87
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Best Local S
Matches 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The amino acid of the hepatocyte growth factor (HGF) generated to contain amino acid changes at residues 492-494. (Note - this sequence is not given in the specification but is based on the HGF sequence given in AAR20005). The generated mutant contains the sequence Lys-Gln-Gly-Arg-Thr, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF is translated as single chain protein which is activated to a two chain protein by protease cleavage between residues 494-5, producing the alpha and beta chains. The novel sequence alters the protease recognition site, putatively introducing a Factor Xa recognition site. The novel HGF deriv. (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were generated by point mutations using the oligonucleotides AAT06762-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                           AAR87525
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                                                                                                                                                                                                                                                                                                                                                                           MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                           standard;
                                                                                                                                      CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                                                                                                      QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQ1PNCDMSHGQDC
                                                                                                                                                                                                                                                         QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARKOCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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                                                                                                                    CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                                                YRGNGKN
                                                                                                                                                                                                       YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                  YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
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                                                                                                                                                                              YMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.9%;
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Pred. No. 9.1e-165;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel derivative of hepatocyte growth factor - positions 492-494, for use in treating injured
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QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                                                                             MTCNGESYRGLMDHTESGKI CQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
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                                       YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                     YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                             MTCNGESYRGLMDHTESGK1CQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
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Val to Lys-Gln-Gly-Arg-Val"
                                                                                                                                                                                                                                                                                                                                   99.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor #4 with changes at residues
                                                                                                                                                                                                                                                                                                                                   Score 2601; DB 2;
Pred. No. 9.1e-165;
                                                                                                                                                                                                                                                                                                                       Mismatches
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Best Local Similarity
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                                                                                                                                                                                                The amino acid of the hepatocyte growth factor (HGF) generated to contain amino acid changes at residues 492-494. (Note - this sequence is not given in the specification but is based on the HGF sequence given in AAR20005). The generated mutant contains the sequence Lys-Gln-Gly-Arg-Ile, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF is translated as single chain protein which is activated to a two chain protein by protease cleavage between residues 494-5, producing the alpha and beta chains. The novel sequence alters the protease recognition site, putatively introducing a Factor Xa recognition site. The novel HGF deriv. (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were generated by point mutations using the oligonucleotides AAT06762-5
                                                                                                                                                                          Sequence 728
                                                                                                                                                                                                                                                                                                                                                                                                                Novel derivative of hepatocyte growth factor - comprises a mutation positions 492-494, for use in treating injured blood vessels.
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Misc-difference
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                                                                            ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                        ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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       ARKOCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCOP
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Val to Lys-Gln-Gly-Arg-Ile"
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Pred. No. 9.1e-165;
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 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
                                                          YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                               QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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                               YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                            QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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Search completed: October Job time: 174.465 secs ω 2005, 06:05:50

452

CYTGNPLIPWDYCPISRCEGDTTPTIV

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Result
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Maximum Match 100%
Listing first 45 summaries
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      DB
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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20: /cgn2_6/ptodata/2/pubpaa/US10B_PUB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US10B_PUB.pep:*

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20: /cgn2_6/ptodata/2/pubpaa/US10B_PUB.pep:*

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WS-10-98-309-2
WS-10-926-088A-1
VS-10-926-088A-1
VS-10-926-088A-2
US-10-926-088A-2
US-10-498-332-7
US-10-926-088A-2
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Sequence 2, Appli
Sequence 120, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 2, Appli
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Sequence 1, Appli
Sequence 2, Appli
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sequence 4, Appii	equence 2,	e 134	Sequence 133, App	e 132	e 120	e 119	e 118	e 229	e 2,	e 134	equence 133	equence 132	equence 53,	e 52, App	equence 51, App	e 42,	e 49987,	e 152, Ap	е 8,	e 2, Appl	e 3, Appl	e 12, App	Sequence 4, Appli	e 4, Appl	e 2, Appl	e 2, Appl	e 2, Appl	equence 13, App	e 14,	e 19, App	e 18, App	ce 20,	Sequence 4, Appli

## ALIGNMENTS

US-09-951-629-1

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APPLICANT: NAKAMURA, Toshikazu
TITLE OF INVENTION: Anti-Cancer Agent
FILE REFERENCE: 4373-0101P
CURRENT APPLICATION UNMBER: US/09/951,629
CURRENT FILING DATE: 2001-09-14
PRIOR FILING DATE: 1995-10-28
PRIOR FILING DATE: 1995-10-28
PRIOR APPLICATION NUMBER: PCT/JP96/03105
PRIOR APPLICATION NUMBER: DCT/JP96/03105
PRIOR FILING DATE: 1996-10-23
PRIOR FILING DATE: 1996-10-23
PRIOR APPLICATION NUMBER: US 09/471,032
PRIOR TILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 1
SECTWARE: Patentin version 3.1
SEQ ID NO 1
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Matches
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                                                                                                                                                                 Query Match
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                          LENGTH: 447
                                                                                                                                                  Local Similarity
61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                     99.9%;
ilarity 99.8%;
Conservative
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                                                                                                                                 Score 2601; DB 9;
Pred. No. 1.1e-211;
1; Mismatches 0;
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Sequence 2, Application US/10081309

Publication No. US20030012775A1

GENERAL INFORMATION:
APPLICANT: Hoffmann-La Roche Inc.
TITLE OF INVENTION: PEG Conjugates of NK4
FILE REFERENCE: 20859
CURRENT APPLICATION NUMBER: US/10/081,309
CURRENT APPLICATION NUMBER: US/10/081,309
CURRENT FLING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 447
TYPE: PRT
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Matches 446
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                                                                 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                   MTCNGESYRGIMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                                                                                                                                                       WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
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 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
                                                   YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
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                                                                                                                                                                                                                                                                                                                            99.9%;
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Pred. No. 1.1e-211;
1; Mismatches 0;
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LENGTH: 494
TYPE: PRT
ORGANISM: Homo 9
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Publication No. US20050164918A1
GENERAL INFORMATION:
APPLICANT: NAKAMURA TOShikazu
APPLICANT: WATSUMOTO Kunio
APPLICANT: FUKUTA Kazuhiro
TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain
FILE REFERENCE: 2004-1328A/WMC/01736
CURRENT APPLICATION NUMBER: US/10/926,088A
CURRENT FILING DATE: 2004-08-26
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 446; Conservat
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OTHER INFORMATION:
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             CYTGNPLIPWDYCPISRCEGDTTPTIV
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                                                                   YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                      QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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CYTGNPLIPWDYCPISRCEGDTTPTIV
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nilarity 99.8%;
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Pred. No. 1.3e-211;
1; Mismatches 0;
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RESULT 4
US-10-872-198-120
; Sequence 120, Application US/10
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS

US/10872198

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RESULT 5
US-11-021-951-120
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PRIOR APPLICATION NUMBER: 60/543,518
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 0403058
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR FILING DATE: 2003-11-11
PRIOR FILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-06-18
Sequence 120, Application US/11021951
Publication No. US20050175581A1
GENERAL INFORMATION:
APPLICANT: HAUPTS, Ulrich
APPLICANT: KOLTERMANN, Andre
APPLICANT: SCHEIDIG, Andreas
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Best Local S
Matches 446
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SEQ ID NO 120
LENGTH: 726
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2004-06-18
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B OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF

REFERENCE: 04156.0002U4
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Andreas SCHEIDIG
Christian VOETSMEIER
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APPLICANT: VOTSMEIER, Christian
APPLICANT: Kettling, Ulrich
APPLICANT: CCCO, Wayne Michael
ITILE OF INVENTION: New Biological Entities And The
ITILE OF INVENTION: And Diagnostic Use Thereof
FILE REFERENCE: 04156.0002U5
CURRENT APPLICATION NUMBER: US/11/021,951
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: 10/872,198
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/543,518
PRIOR APPLICATION NUMBER: 60/543,518
PRIOR APPLICATION NUMBER: 60/544,960
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-06-18
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SOFTWARE: PatentIn ver
SEQ ID NO 120
LENGTH: 726
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Best Local (
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Pred. No. 2e-211;
1; Mismatches
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RESULT 6
US-08-605-221-2
US-08-605-221-2
; Sequence 2, Application US/08605221
; Publication No. US20030060403A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Toshikazu

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; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3
; SEQ ID NO 10
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-813-805-10
                                                                                                                                               Sequence 10, Application US/10813805
Publication No. US20040191902A1
GENERAL INFORMATION:
APPLICANT: PFIZER INC.
APPLICANT: Hambor, John E.
APPLICANT: Hambor, John E.
APPLICANT: Roach, Marsha L.
TITLE OF INVENTION: GROWTH AND DIFFERENTIATION OF
FILE REFERENCE: PC25028A
CURRENT FILING DATE: 2004-03-30
PRIOR APPLICATION NUMBER: US/10/813,805
PRIOR APPLICATION NUMBER: US 60/459,449
PRIOR FILING DATE: 2003-03-31
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CURRENT FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 728
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: HGF-A (Full length HGF)
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US-10-813-805-10
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FILE REFERENCE: 2520-0101P
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Pred. No. 2e-211;
1; Mismatches
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APPLICANT: Gherardi, Ermanno
APPLICANT: Lietha, Daniel
APPLICANT: Lietha, Daniel
APPLICANT: Lietha, Daniel
APPLICANT: Chirgadze, Dimitry Y
TITLE OF INVENTION: The NK1 Fragment of Hepatocyte Growth Factor/Scatter
TITLE OF INVENTION: Factor (HGF/SF) and Variants Thereof, and Their Use
FILE REFERENCE: 2502489-991180
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: US/10/475,616
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: GEOT/GB02/01941
PRIOR APPLICATION NUMBER: GB 0110430.6
PRIOR FILING DATE: 2001-04-29
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 728
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                                                                                                                                               Matches 446;
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ORGANISM: Homo
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                 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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1; Mismatches
                                                                                                                                             Score 2601; DB 16;
Pred. No. 2e-211;
1; Mismatches 0;
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FILE REFERENCE: 14539-016US1
CURRENT APPLICATION NUMBER: US/10/498,332
CURRENT FILING DATE: 2004-06-11
PRIOR APPLICATION NUMBER: PCT/JP02/13014
PRIOR APPLICATION NUMBER: PCT/JP02/13014
PRIOR FILING DATE: 2002-12-12
PRIOR FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: JP 2001-380158
PRIOR APPLICATION NUMBER: JP 2001-380158
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 57
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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US-10-498-332-7
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Best Local S
Matches 446
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Publication No. US20050113284A1
GENERAL INFORMATION:
APPLICANT: Nakamura, Motonao
APPLICANT: Higuchi, Toshio
APPLICANT: Yamasaki, Yoshiki
APPLICANT: Orita, Takuya
TITLE OF INVENTION: PHARMACEUTICAL AGENTS AND METHODS FOR
TITLE OF INVENTION: TISSUE AND VASCULAR REGENERATION
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US-10-149-103A-1
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Best Local S
Matches 438
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APPLICANT: Sim, Kim Lee
APPLICANT: Sim, Clara
APPLICANT: Day, Clara
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
FILE REFERENCE: 05213-0592 43170-274540
CURRENT APPLICATION NUMBER: US/10/149,103A
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/US00/34039
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 727
TYPE: PRT
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Local Similarity 98.2%;
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                                                                                                                         YPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCY
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Pred. No. 2.3e-208;
6; Mismatches 2;
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Length Indels

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US-08-605-221-4
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US-10-926-088A-2
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Publication No. US20050164918A1
GENERAL INFORMATION:
APPLICANT: NAKAMURA Toshikazu
APPLICANT: MATSUMOTO Kunio
APPLICANT: FUKUTA Kazuhiro
APPLICANT: FUKUTA Kazuhiro
APPLICANT: FUKUTA Kazuhiro
APPLICANT: 5004-1328A/WMC/01736
CURRENT APPLICATION NUMBER: US/10/926,088A
CURRENT APPLICATION NUMBER: US/10/926,088A
CURRENT FILING DATE: 2004-08-26
NUMBER OF SEQ ID NOS: 6
                                                                  Sequence 4, Application US/08605221
Publication No. US20030060403A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 441; Conserv
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APPLICANT: NAKAMURA, Toshikazu
TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER
FILE REFERENCE: 2520-0101P
CURRENT APPLICATION NUMBER: US/08/605,221
CURRENT FILING DATE: 1996-03-15
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ORGANISM: Homo Sapiens
FEATURE:
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98.7%;
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Pred. No. 1.9e-208;
1; Mismatches 0; 1
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; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: HGF-B (five
US-08-605-221-4
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US-10-509-247A-20
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APPLICANT: Japan Sci
APPLICANT: Kuroda,
APPLICANT: Tanizawa
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SOFTWARE: PatentIn Ver.
SEQ ID NO 4
                                                         SOFTWARE: PatentIn version 3.3 SEQ ID NO 20
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                                                                                           CURRENT APPLICATION NUMBER: US/10/509,247A
CURRENT FILING DATE: 2004-09-28
PRIOR APPLICATION NUMBER: PCT/JP03/02602
PRIOR FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: JP2002-97280
PRIOR APPLICATION NUMBER: JP2002-97280
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                            APPLICANT: Kondo, Akihiko
APPLICANT: Ueda, Masakazu
APPLICANT: Seno, Masakazu
APPLICANT: Tada, Hiroko
TITLE OF INVENTION: DRUG CONTAINING HOLLOW PROTEIN NANOPARTICLES OF PARTICLE-FORMING
TITLE OF INVENTION: PROTEIN, FUSED WITH DISBASE-TREATING TARGET-CELL-SUBSTANCE
FILE REFERENCE: P033P01/US
                   LENGTH: 1109
TYPE: PRT
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Kondo, Akihiko
                                                                                                                                                                                                                                                                                                                                                                                Kuroda, Shunichi
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Sequence
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RESULT 14
US-10-133-912-18
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; OTHER INFORMATION: Synthetic Construct
US-10-509-247A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application Publication No. US20020 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.7
Best Local Similarity 98.7
Matches 441; Conservative
COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/5 inch diskette
MEDIUM TYPE: 3 1/5 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: WORD FOR WINDOWS
SOFTWARE: MICROSOFT WINDOWS 98
CURRENT APPLICATION NUMBER: US/10/133,912
APPLICATION NUMBER: US/10/133,912
FILING DATE: 25-Apr-2002
CLASSIFICATION - 25-Apr-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/700,519
                                                                                                                                                                                                                     Ueda, Masatsugu
Higashio, Kanji
Yamashita, Yasushi
TITLE OF INVENTION: TCF MUTANT
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSSE: Burgess, Ryan and Wayne
STREET: 370 Lexington Avenue, Suite 21
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
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                                                                                                                                                                                                          ZIP: 10017
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No. US20020165358A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinosaki, Masahiko
Yamaguchi, Kyoji
                                                                                                                                                                                                                                                                                                                                                                                                                            Murakami, Akihiko
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98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Masaaki
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Pred. No. 5e-208;
1; Mismatches
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TOPOLOGY: LINEAR
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-133-912-18
                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-133-912-19
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                                                                                                                                                                                                                                       Sequence 19, Application US/10133912
Publication No. US20020165358A1
GENERAL INFORMATION:
APPLICANT: Kinosaki, Masahiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-683-8150
TELEPAX: 212-532-4285
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 723
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                         Ueda, Masatsugu
Higashio, Kanji
Yamashita, Yasushi
TITLE OF INVENTION: TCF MUTANT
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milcon J.
REGISTRATION NUMBER: 17,9
                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        452
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                                                                                                                                                                                                                                                                                                                                                                                      PLIPWDYCPISRCEGDTTPTIV 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG
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                   STREET: 370 Lex
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
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                                                       ADDRESSEE: Burgess,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                    Goto, Masaaki
                                                                                                                                                                                   Murakami, Akihiko
                                                                                                                                                                                                                     Yamaguchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG
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98.9%;
                                      Lexington Avenue,
                                                                                                                                                                                                                     Куојі
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                                                       Ryan and
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Pred. No. 2.26
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                                        Suite
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391 365 331 305 245 211 185

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TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-133-912-19
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FILING DATE: 26-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milton J.
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-5240PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-683-8150
TELEPHONE: 212-683-8150
TELEPAX: 212-532-4285
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.5%; Score 2539.5; Best Local Similarity 97.8%; Pred. No. 3.2e-Matches 437; Conservative 1; Mismatches
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APPLICATION NUMBER: US/10/133,912
FILING DATE: 25-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/5 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: WORD FOR WINDOWS
SOFTWARE: MICROSOFT WINDOWS 98
                                                                                                 361
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447
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               CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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                                                                                   YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
                                                                                                                                 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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                                                                                                                                                                                                                       YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
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CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
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473
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Search completed: October Job time: 243.355 secs

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2005, 07:42:28

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
6: /cgn2_6/ptodata/1
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-460-890A-50
US-08-167-641C-50
US-08-167-971A-50
US-08-462-040-50
US-08-462-040-50
US-08-605-221-2
US-08-601-040A-27
US-09-601-040A-27
US-09-601-040A-8
US-07-838-410-1
US-08-290-937B-1
US-08-290-937B-1
US-08-290-937B-2
US-08-1040A-10
US-08-1040A-10
US-08-1040A-10
US-08-1040A-10
US-08-1040A-10
US-08-1040A-10
US-09-601-040A-10
US-08-290-937B-3
US-08-290-937B-3
US-08-290-937B-3
US-08-290-937B-3
US-08-290-937B-3
US-08-290-937B-3
US-08-1040A-10
US-08-290-937B-3
US-08-1040A-10
US-08-290-937B-3
US-08-1040A-10
US-08-290-937B-3
US-08-1040A-10
US-08-290-937B-3
US-08-1040A-10
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              Sequence 50, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appli
Sequence 27, Appl
Sequence 27, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
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US-08-460-890A-50
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Result

45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29	28
1059	1059	1059	1059	1066	1125	1125	1180.5	1180.5	1180.5	1180.5	1180.5	1180.5	1180.5	1180.5	1180.5	1447.5	1471
40.7	40.7	40.7	40.7	40.9	43.2	43.2	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	55.6	56.5
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US-08-326-785-1	US-08-452-260-1	US-08-451-932-1	US-08-248-629A-1	US-08-991-761A-13	US-09-296-219-1	US-08-766-982-1	PCT-US95-13830-2	US-09-949-016-6981	US-09-601-040A-12	US-09-600-991-20	US-09-296-219-2	US-08-766-982-2	US-08-666-082B-1	US-08-334-177-2	US-08-184-012C-8	US-09-600-991-4	US-08-484-841A-8
Seguence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 13, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 6981, Ap	Sequence 12, Appl	Sequence 20, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 8, Appli

## ALIGNMENTS

Minimum DB Maximum DB

Searched:

Scoring table:

Title: Perfect score:

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Sequence 50, Application US/08460890A Patent No. 5994109
GENERAL INFORMATION:
                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: 97/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: 33,327
REGISTRATION NUMBER: 33,327
REGISTRATION NUMBER: 33,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 212/066
TELEPAN: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRAI
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                       SEQUENCE CHARACTERISTICS:
LENGTH: 697 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California COUNTRY: U.S.A.
STRANDEDNESS:
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90071-2066
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RESULT 2
US-08-167-641C-50
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; MOLECULE TYPE: peptide
US-08-460-890A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Appli
Patent No. 6033884
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: WOO, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MCILBIC ACID TRANSPORTER SYSTEMS ITTLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5
SOFTWARE: FastSEQ for Windows 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,64
FILING DATE: December 14, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A. ZIP: 90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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    Mismatches

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Pred. No. 2.7e-214;
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                                         GENERAL INFORMATION:

APPLICANT: WOO, Savio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Cristiano, Richard

APPLICANT: Gottchalk, Stephen

TITLE OF INVENTION: NUCLEIC A

TITLE OF INVENTION: METHODS OI

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ANDRESSESSE
                                                                                                                                                                                                  Sequence 50, Application US/08460971A Patent No. 6150168
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Best Local (
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TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 697 amino acids
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 STREET:
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               3: Lyon & Lyon
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.k, Stephen
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Pred. No. 2.7e-214;
1; Mismatches 0;
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Length 697;

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Best Local Similarity 99.8%;
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OPERATING SYSTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: Unne 5, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 07/855,389
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: MArch 19, 1993
APTLING DATE: MARCH 19, 1993
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 697 amino acids
TYPE: amino acid
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
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CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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212/063
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Sequence 50, Application US/08462040
Patent No. 6177554
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRAN
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
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Best Local Similarity
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COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FASTSEQ for Windows 2.0

CURRENT APPLICATION NUMBER: US/08/462,040

FILING DATE: June 5, 1995

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/167,641

APPLICATION NUMBER: 07/855,389

FILING DATE: March 20, 1992

APPLICATION NUMBER: POT/US93/02725

FILING DATE: March 19, 193

APPLICATION NUMBER: DOSSON

INAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 212/078

TELEPAN: (213) 489-1600

TELEPAN: (213) 955-0440
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: si
TOPOLOGY: linear
MOLECULE TYPE: pep
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STREET: 633 West Fifth
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 697 amino acids
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                                                           WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGFWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                             ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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                                      WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
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                                                                                                                                                                                                                                                            Score 2601; DB 3;
Pred. No. 2.7e-214;
1; Mismatches 0;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-815-333A-2
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US-07-815-333A-2
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 446; Conserv
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Patent No. 5342831
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APPLICANT: Nakamura, Toshikazu

APPLICANT: Matsumoto, Kunio

TITLE OF INVENTION: EPITHELIOCYTE GROWTH ACCELERATOR
                                                                                                                                                                                                                                                                                                                                     TELEFAX: (312) 616-570
TELEX: 25-3533
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19911227
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Green, Robert F.
REGISTRATION NUMBER: 27555
REFERENCE/DOCKET NUMBER: 4406
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 616-5600
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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ADDRESSEE: Leydig, Voit & Mayo
STREET: Two Prudential Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/815,333A
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                      ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                        ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
                    ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                      QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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Best Local Similarity
Matches 446; Conserv
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,783A
FILING DATE: 13-Jul-1993
CLASSIFICATION -435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
ANAME: MATSGRANG, DIAME L.
                                 Query Match
                                                                                                                                  TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                         NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: PO-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
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CITY: South San Francisco
STATE: California
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                                                                                        TOPOLOGY:
                                                                                                                     LENGTH:
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              99.9%;
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Score 2601; DB 1;
Pred. No. 2.9e-214;
1; Mismatches 0;
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Sequence 2, Application US/08605221

; Patent No. 6699837
; GENERAL INFORMATION:
    APPLICANT: NAKAMURA, Toshikazu
    TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
    FILE REFERENCE: 2520-0101P
; CURRENT APPLICATION NUMBER: US/08/605,221
; CURRENT FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: HGF-A (Full length HGF)
US-08-605-221-2
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                       MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
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CYTGNPLIPWDYCPISRCEGDTTPTIV
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                                                                                                                                                                                                    Score 2601; DB 4;
Pred. No. 2.9e-214;
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GENERAL INFORMATION:
APPLICANT: MEDICO, Enzo et al.
APPLICANT: MEDICO, Recombinant Proteins from HG
FILE REFERENCE: 0471-0161P
CURRENT APPLICATION NUMBER: US/09/601,040A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 27
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US-09-601-040A-27
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TYPE: PRT
ORGANISM: Homo :
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Pred. No. 2.8e-211;
1; Mismatches 0;
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Sequence 6, Application US/09601040A

Patent NO. 6730657;
GENERAL IMPORMATION:
APPLICANT: MEDICO, Enzo et al.
TITLE OF INVENTION: Recombinant Proteins from HGF and MSP FILE REFERENCE: 0471-0161P;
CURRENT APPLICATION NUMBER: US/09/601,040A;
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 717
TYPE: PRT
ORGANISM: Artificial Sequence
CURRENT APPLICATION NUMBER: US/09/601,040A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 717
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-601-040A-8
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MEDICO, Enzo et al.
TITLE OF INVENTION: Recombinant Proteins
FILE REFERENCE: 0471-0161P
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Best Local Similarity
Matches 441; Conserv
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98.7%;
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Pred. No. 4.6e-211;
1; Mismatches 0;
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RESULT 11
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APPLICANT: SHIMA, NOBUYUKI
                                                         ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         APPLICANT: OOGAKI, FUMIKO
APPLICANT: TAKAOKA, HIROAKI
APPLICANT: TSUDA, EISUKE
TITLE OF INVENTION: PLASMIDS CONTAINING DNA ENCODING THE
TITLE OF INVENTION: AMINO ACID SEQUENCE OF TCF-II, TRANSFORMED CELLS WITH THE
TITLE OF INVENTION: PLASMIDS, AND PRODUCTION MEDITHOD OF BIOLOGICALLY ACTIVE
TITLE OF INVENTION: SUBSTANCE USING THE TRANSFORMED CELLS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
PRIOR APPLICATION DATA:
               APPLICATION NUMBER: UFFILING DATE: 19920311 CLASSIFICATION: 435
                                                                                                                                                            COUNTRY: U
                                                                                                                                                                                                            STREET: 2200 CL
CITY: ARLINGTON
                                                                                                                                                                                              STATE:
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NAGAO, MASAYA
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98.7%;
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Pred. No. 4.6e.
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ismatches 0;
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US-07-838-410-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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Best Local
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REGISTRATION NUMBER: 17,746
REFERENCE/DOCKET NUMBER: WAN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
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MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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LOCATION: 605..623
OTHER INFORMATION: /
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TELEFAX: 64191
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LOCATION: 490..505
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 393..405
OTHER INFORMATION: OTHER INFORMATION:
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CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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98.7%;
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SEQUENCE IN ALPHA-CHAIN"
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SEQUENCE IN BETA-CHAIN"
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Pred. No. 4.7e-211;
1; Mismatches 0;
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US-08-290-937B-1
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                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: YAMAGU
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,937B
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: MODIFIED
NUMBER OF SEQUENCES: 13
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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STREET: 125 High St.
                                                                                                                                                                                                                                                                                      Local Similarity
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MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
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TAKAHIRA, REIKO
OOGAKI, FUMIKO
UEDA, MASATSUGU
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GOTO, MASAAKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                    98.4%;
98.7%;
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                                                               SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
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                                                                                                                                                                                                                                                                                    Score 2563.5; DB 1
Pred. No. 4.7e-211;
                                                                                                                                                                                                                                                                      Mismatches
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US-08-290-937B-2
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                                                                        Query Match
Best Local Similarity
                                                             Matches 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YAMAĞUCHI, KYOJI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: MURAKAMI, AKIHIKO
APPLICANT: GOTO, MASAAKI
APPLICANT: TSUDA, EISUKE
APPLICANT: TAKAHIRA, REIKO
APPLICANT: TAKAHIRA, REIKO
APPLICANT: UEDA, MASATSUGU
APPLICANT: UEDA, MASATSUGU
APPLICANT: UEDA, MASATSUGU
APPLICANT: HIGASHIO, KANJI
TITLE OF INVENTION: MODIFIED TCF
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                          TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       APPLICATION UMBER: US/08/290
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-
TELECOMMUNICATION INFORMATION:
                                                                                                                                      LENGTH: 723 amino acids
TYPE: amino acid
STRANUBENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91
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125 High St.
                                                               Conservative
                                                                          98.4%;
98.7%;
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                                                          Score 2563.5; DB 1;
Pred. No. 4.7e-211;
Mismatches 0;
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                                                             Indels
                                                                                       Length 723;
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US-08-404-643-1
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COUNTRY: USA
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2
SOFTWARE: PatentIn Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,643
FILING DATE: 15-MAR-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
ARGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-034 (3999/35)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)-248-7100
INFORMATION FOR SEQ ID NO: 1:
CECULARY FOR SEQ ID NO: 1:
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Patent No. 5658742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: HIGASHIO, KANJI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: OOGAKI, FUMIKO
TITLE OF INVENTION: MONOCLONAL ANTIBODY
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA,
TOPOLOGY: 11
                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
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CITY: BOSTON
                                                      STRANDEDNESS:
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                                                                               amino acid
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                                                   single
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Sequence 1, Application US/09194326
Patent No. 6306827
GENERAL INFORMATION:
APPLICANT: Kinosaki, Masahiko
APPLICANT: Masanuga, Hiromi
APPLICANT: Masanuga, Hiromi
APPLICANT: Masanuga, Hiromi
APPLICANT: Higashio, Kanji
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Agent for Preventing and/or Tre.
FILE REFERENCE: FJN-069
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: US/09/194,326
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: PT/JP98/01221
EARLIER APPLICATION NUMBER: JP 94989
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATEND DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATEND SAPIENS
FEATURE:
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: TCF-II
US-09-194-326-1
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US-09-194-326-1
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                                                     Query Match
Best Local Similarity
Matches 441; Conserv
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Best Local Similarity 98.7%;
Matches 441; Conservative
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                                                       Conservative
                                                               98.4%;
                                                    Score 2563.5; DB 3;
Pred. No. 4.7e-211;
1; Mismatches 0;
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1; Mismatches 0;
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Search completed: October 3, 2005, 06:53:48
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Title:
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2579
1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 442
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	ი	5	4	ω	2	_	Result No.
270	291	302	302.5	344	350	352.5	353	357.5	406	450.5	457	840	864.5	927	1018.5	1019.5	1021	1036	1039.5	1054.5	1114.5	1133.5	1171	1750	1830	2363.5	2370.5	563.	Score
10.5	11.3	11.7	11.7	13.3	13.6	13.7	13.7	13.9	15.7	17.5	17.7	2	w	35.9	9	9	39.6	•	0	40.9	٠	44.0	45.4		71.0	91.6	91.9	•	Query Match
120	559	559	562	617	622	618	169	625	336	455	460	1420	4548	2869	810	812	810	810	812	790	716	716	711	411	710	728	728	728	Length
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E61545	A29941	A35029	UKHUT	S10511	TBHU	A35827	A40522	TBBO	S33879	A61545	B61545	A32869	S00657	T18518	PLHU	PLBO	B30848	I46260	PLMS	PLPG	A40332	JC5061	A47136	I51285	151283	A35644	A60185	JH0579	ID
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45	44	3	42	41	40	39	8	37	36	35	34	S S	32	31	30
158	158.5	158.5	182.5	186.5	189	192.5	200	204	213.5	225	228.5	236.5	237.5	260.5	268
6.1	6.1	6.1	7.1	7.2	7.3	7.5	7.8	7.9	8.3	8.7	8.9	9.2	9.2	10.1	10.4
442	685	433	806	560	593	558	615	655	937	291	603	943	946	89	123
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UKPG	A48289	JN0560	T18840	JC4795	S45281	JC5878	KFHU12	A46688	A45082	I38098	S28941	B45082	A47299	A60140	C61545
u-plasminogen acti	neurotrophic recep	u-plasminogen acti	hypothetical prote	plasma hyaluronan-	coagulation factor	plasma hyaluronan-	coagulation factor	hepatocyte growth	neurotrophic recep	t-plasminogen acti	coagulation factor	neurotrophic recep	ror-related recept	plasmin (EC 3.4.21	plasmin (EC 3.4.21

## ALIGNMENTS

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A; Note:
C; Superf
                                                                                                      A;Map position: 7q21.1-7q21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; C;Complex: disulfide-bonded heterodimer of chains derived C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034 R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N. Eur. J. Biochem. 197, 15-22, 1991 A;Title: An alternatively processed mRNA generated from human hepatocyte A;Reference number: S15443; MUID:91200041; PMID:1826653 A;Accession: S15443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the authors translated the codon CAG for residue 727 as Glu A;Note: part of this sequence, including the amino end of both the alpha and beta R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte grown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 86-91,329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546, R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Nature 342, 440-443, 1989
A;Title: Molecular cloning and expression of human hepatocyte growth factor.
A;Reference number: S06794; MUID:90066676; PMID:2531289
A;Accession: S06794
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A;Residues: 32-43;53-58 <YOS>
A;Residues: 32-43;53-58 <YOS>
A;Residuer: Diasma
R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990
A;Title: Scatter factor: molecular characteristics and effect on A;Reference number: A37796; MUID:91035621; PMID:2146276
A;Accession: A37796
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R;Yoshiyama, Y; Arakaki, N: Naka, D; Takahashi, K.; Hirono, S.; Kondo, J.; Nakaya
Biochem. Biophys. Res. Commun. 185, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy chain of both native
A;Reference number: PH0114; MUID:91207365; PMID:1826837
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                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 161-166 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084 R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K. Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991 A;Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibr A;Reference number: I52253; MUID:92062058; PMID:1835383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL;X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
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                                                                      A; Description: stimulates mitosis of hepatocytes and other
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated
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A; Residues: 1-288, 'ET' <MIY2>
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                                                                                                                                                                                                                                        Cross-references: GDB:127524; OMIM:142409
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                                      have proteinase
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activity
factor/macrophage stimulating protein
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                                                                                                                                         347/2; 390/1; 424/2; 469/1; from the same precursor
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   kringle
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C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr. F;13-31/Domain: signal sequence #status predicted <SIG> F;32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT> F;32-494/Domain: alpha chain #status experimental <ACH> F;128-206/Domain: kringle homology <KR1> F;211-288/Domain: kringle homology <KR2> F;305-383/Domain: kringle homology <KR3> F;391-469/Domain: kringle homology <KR3> F;391-469/Domain: kringle homology <KR4> F;495-728/Domain: beta chain #status experimental <BCH> F;495-728/Domain: trypsin homology <TRY> F;495-716/Domain: trypsin hom
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                                                                                                                                               CYTGNPLIPWDYCPISRCEGDTTPTIV
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Pred. No. 1.6e-175;
1; Mismatches 0;
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hepatocyte growth factor precursor - mouse
NyAlternate names: hepapoietin A; Scatter factor
C;Species: Mus musculus (house mouse)
C;Jate: 03-Mar-1993 #sequence revision 26-May-1994 #text\_change 09-Jul-2004
C;Accession: JC2117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; JU0231
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
Biochem. Blophys. Res. Commun. 199, 772-779, 1994
A;Title: Identification of mouse mammary fibroblast\_derived mammary growth factor a A;Molecule type: mRNA A;Residues: 1-728 <SAS2> A;Cross-references: UNIPROT:QO8048; GB:D10212; A;Experimental source: fibroblast, COS-1 cell A;Note: submitted to JIPID, May 1993 R;Rosen, A; Molecule type: protein A; Residues: 496-504 <SA2> A; Accession: PC2064 A;Reference number: JC2117; MUID:94183257; PMID:8135822 A;Accession: JC2117 E.M.; Meromsky, Setter, [F] . Vinter, NID:g220435; D. ₩., Goldberg, PIDN:BAA01064.1;

PID:g220436

Soc.

Biol.

Med.

195,

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A;Molecule type: protein
A;Residues: 496-507, 'X., 509-512,'I', 514-516,'X', 518-519 < NAT>
A;Residues: 496-507, 'X., 509-512,'I', 514-516,'X', 518-519 < NAT>
R;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
J. Biol. Chem. 270, 830-836, 1995
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Residues: 1-30 < RES
A;Cross-references: EMBL:X81630; NID:g673451; PIDN:CAA57286.1; PID:g673452
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Function:
A;Poscription: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homology c;Superfamily: hepatocyte growth factor/macrophage stimulating protein; kringle homology c;Superfamily: hepatocyte growth factor alpha chain #status predicted c;Mar>
F;56-495, 496-728/pomain: kringle homology c;RR3>
F;305-384/pomain: kringle homology c;RR3>
F;305-384/pomain: kringle homology c;RR3>
F;305-384/pomain: kringle homology c;RR3>
F;305-384/pomain: kringle homology c;RR3>
F;306-719/pomain: kringle hom
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A,Accession: S45521
A;Status: prelicity
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R;Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.
Biochem. J. 278, 35-41, 1991
A;Title: Purification and characterization of biologically
A;Reference number: S17173; MUID:91354223; PMID:1831975
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A;Status: prelimina
A;Molecule type: pr
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A;Molecule type: protein
A;Residues: 496-517,'T',519 <COF>
R;Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
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A;Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377,'E',379,
R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
Biochim. Biophys. Acta 1216, 299-303, 1993
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A; Reference number: S10966; MUID:90326152; PMID:2142751
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A; Residues: 1-563,'H',565-728 <LI2>
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A; Residues: 1-728 < LII
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                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                         ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                      QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK
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                                                                                                                                                                                                                                                                                         Score 2370.5; DB 1;
Pred. No. 9.9e-162;
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A; Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle ho
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
F;66-495/Domain: signal sequence #status predicted <SIG>
F;66-495/Domain: hepatocyte growth factor #status predicted <ACH>
F;129-207/Domain: kringle homology <KR1>
F;129-207/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR3>
F;302-470/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: kringle homology <KR4>
F;496-719/Domain: kringle homology <KR4>
F;496-719/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: kringle homology <TRY>
F;496-719/Domain: krypsin homology <TRY>
F;496-719/Domain: krypsin homology <TRY>
F;495-403,559,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                          176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                                                                  356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                                                        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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                      CYTGNPLIPWDYCPISRCEGDTTPTIV 442
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CYTGNELIPWDYCEISRCEGDTTETIV
                                                                                                                                   QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC
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                                                                    YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW
                                                                                                                                                                                                    YTLDPDTPWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS
                                                                                                                                                                                                                                   YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
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Eur. J. Blochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte growth factor A;Reference number: S13211; MUID:91031482; PMID:2146117
A;Accession: S13211
A;Status: preliminary
                                                                                                                                                         A;Cross-references: UNIPROT:P17945; GB:D90102; GB:M32987; NID:g220766; PIDN:BAA14133.1; A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417 R;Okajima, A.; Miyazawa, K.; Kitamura, N.
                                                                                                                                                                                                                                                                                                                                                    R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor A;Reference number: A35644; MUID:90222197; PMID:2139229
A;Accession: A35644
                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <TAS>
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Accession: A35644; S13211
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A;Molecule type: mRNA
A;Residues: 1-728 <ORA;
A;Residues: 1-728 <ORA;
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
A;Cromplex: disulfide-bonded heterodimer of chains derived from the same pr

protein 1; kringle homolo heterodimer; kringle; pyr

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Gaps

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A;Note: does not have proteinase activity
C;Superfamily: hepatrocyte growth factor/macrophage stimulating protein 1; k
C;Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle
F;42-477,478-709/Product: hepatrocyte growth factor #status predicted <AAT>
F;415-193/Domain: hepatrocyte growth factor alpha chain #status predicted <AC
F;115-193/Domain: kringle homology <KR1>
F;198-275/Domain: kringle homology <KR3>
F;289-367/Domain: kringle homology <KR3>
F;375-453/Domain: kringle homology <KR4>
F;478-709/Domain: kringle homology <KR4>
F;478-709/Domain: hepatrocyte growth factor beta chain #status predicted <BC
F;478-700/Domain: trypsin homology <TRY>
F;52,128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent
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I51283
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                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:S77422; NID:g998932; PIDN:AAB34354.1; PID:g998933 A;Note: the authors' translation for residue 458 (Thr) is inconsistent with the C;Complex: disulfide-bonded heterodimer of chains derived from the same precurson.
                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-710 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                      Mech. Dev. 49, 123-131, 1995
A;Title: Molecular cloning of Xenopus HGF cDNA and its expression
A;Reference number: I51283; MUID:95267690; PMID:7748783
A;Accession: I51283
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3; Mismatches 20;
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C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text
C; Accession: IS1285
R; Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Ap:
Development 121, 813-824, 1995
A; Title: A role for HGF/SF in neural induction and its 6
A; Reference number: IS1285; MUID:95237013; PMID:7720585
A; Accession: IS1285
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                       SMIPHEHS-----YRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS
                                                        SMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGES
                                                                                                           KQCLWFPFNSMSSGVKXEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS
                                                                                                                                                                                  KRRNPLHDYKKTGELMLIKVNKTLEVKTKLLNTTEQCAKRCSRNKGLSFTCKAFAYDRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGNPLIPWDYCPISRCEGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNGEHYRGPMDYTESGKECORWDLORPHKHKFRPERYPNKGLNDNYCRNPDGKSRPWCYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMIPHEHSFLPSTYRGKDLKENYCRNPKGEEGGPWCFTKSPEVRHDVCDIPFCSEVDCVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNGSTYKGTLSRTRFRLPCSMWEKNLQDLKRHTFNEPDVSILQKNYCRNPDNDAHGPWCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHIHNFTPENYKCKDLSENYCRNPDGSESPWCFTTDPNIRIGHCSQIKKCQASNQQECYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDPDTSWEFCAIKPCVHSIVNNTDI----TKDCMKGQGEGYRGSVSTTYNGIQCQRWDSQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRCHWFSFNTMSAGIKDKYDISFDLYEKKDYIRDCIHGKGSNYRGTRNVTKRGLACQPWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKRNAFDDYKKTAETTLTRLNKALEVKTKMFNTTENCAKRCSRNKGLPFTCKAFAFDKNI
   YRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         translated
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75.9%;
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3; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                                                        Score 1750; DB 2;
Pred. No. 1.1e-117;
7; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                           Length 411;
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Sharpe, M.J.;

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Gaps

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242

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89

09-Jul-2004

437 417 377 317 297 237

200

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A;Reference number: A61395; MUID:91217635; PMID:1827141
A;Accession: A61395
A;Molecule type: protein
A;Residues: 230-247;288-291, 'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291, 'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291, 'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291, 'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Residues: 230-247;288-291,'X',297-301,'X',303,'E',305,'EX',305,'EX',305,'EX',305,'EX',305,'EX',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'X',297-301,'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macrophage-stimulating protein 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 14-Nov-1997 #text_ch
C;Date: 03-May-1994 #sequence_revision 14-Nov-1997 #text_ch
C;Accession: A40331; B40331; A47136; A61395
R;Han, S.; Stuart, L.A.; Degen, S.J.F.
Biochemistry 30, 9768-9780, 1991
A;Title: Characterization of the DNF1582 locus on human chr
A;Reference number: A40331; MUID:92002016; PMID:1655021
A;Reference number: A40331; MUID:92002016; PMID:1655021
A;Accession: A40331
A;Molecule type: DNA
A;Residues: 1-711 <HA1>
A;Cross-references: UNIPROT:P26927; GB:M74179
A;Accession: B4031
A;Accession: B4031
A;Residues: 1-711 <HA2>
A;Cross-references: GB:M74178; NID:9183976; PIDN:AAA50165.1
A;Cross-references: GB:M74178; NID:9183976; PIDN:AAA50165.1
A;Cross-references: GB:M74178; NID:9183976; PIDN:AAA50165.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Cloning, sequencing, and expression of human macrophage stimulating pr A;Reference number: A47136; MUID:93340141; PMID:8393443
A;Accession: A47136
A;Molecule type: mRNA
A;Residues: 1-12,'C',14-622,'F',624-711 <YOS>
A;Cross-references: GB:L11924; NID:9398037; PIDN:AAA59872.1; PID:9398038
A;Note: authors translated the codon TTT for residue 623 as Leu; parts of this A;Note: authors translated the codon TTT for residue 623 as Leu; parts of this R;Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, J. Exp. Med. 173, 1227-1234, 1991
A;Title: Macrophage stimulating protein: purification, partial amino acid seque A;Reference number: A61395; MUID:91217635; PMID:1827141
                                                                                                                               F;110-186/Domain: kringle homology <KR1>
F;191-268/Domain: kringle homology <KR2>
F;283-361/Domain: kringle homology <KR2>
F;283-361/Domain: kringle homology <KR4>
F;370-448/Domain: kringle homology <KR4>
F;484-711/Domain: beta chain #status predicted <BCH>
F;484-711/Domain: beta chain #status predicted <BCH>
F;484-704/Domain: trypsin homology <TRY>
F;464-704/Domain: trypsin homology <TRY>
F;56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37
F;72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           á
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                                    Similarity
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                                45.48;
   60;
                                Score 1171;
Pred. No. 4
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       Mismatches
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                                    .4e-76;
                                                                     DB 1;
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                                                             Length 711;
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A. Title: Molecular cloning of rat macrophage-stimulating protein and its involvements. A; Reference number: JC5061; MUID:97011126; PMID:8858136
A; Reference number: JC5061
A, Holecule type: mRNA
A; Residues: 1-716 < OHS
A; Cross-references: UNIPROT:P70521; EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; P. A; Cross-references: UNIPROT:P70521; EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; P. Cross-references: UNIPROT:P70521; Embl:X950996; NID:g1669718; PIDN:CAA64473.1; P. Cross-references: UNIPROT:P70521; EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; P. Cross-references: UNIPROT:P70521; PIDN:G169718; PIDN:G1
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jar
C;Accession: JC5061
R;Ohshiro, K; Iwama, A.; Matsuno, K.; Ezaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ś
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          GPWCYTTNRSVRFQSCGIKSCREAVCVWCNGEDYRGEVDV
                                                                                                                                             YVRTCIMDNGASYRGTVARTADGLPCQAWSRRFPNDHKYTPTPKNGLEENFCRNPDGDPR
                                                                                                                                                                                                           YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR---GKDLQENYCRNPRGEEG
                                                                                                                                                                                                                                                                                VADAEECARRC----GPLLDCRAFHYNMSSHGCQLLPWTQHSLRAQLHHSSLCDLFQKKD
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                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1133.5;
Pred. No. 2.1e.
68; Mismatches
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2.1e-73;
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the same precurso
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A;Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homold C;Keywords: duplication; glycoprotein; growth factor; kringle f;1-31/Domain: signal sequence #status prodicted core.
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A; Residues: 1-18, 'P', 20-716 < DEG2 >
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A; Residues: 1-716 < DEG >
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A;Title: Characterization of the mouse cDNA and gene coding A;Reference number: A40332; MUID:92002017; PMID:1832957
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;489-709/Domain: trypsin homology <TRY>
;72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: A40332; B40332
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                                                                                 GPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKF
                                                                                                                                                                                                                                                     YIRNCIIGKGRSYKGTVSITKSGIKCOPWSSMIPHEHSYR---GKDLQENYCRNPRGEEG
        GPWCYTTNRSVRFQSCGIKTCREAVCVLCNGEDYRGEVDVTESGRECQRWDLQHPHSHPF
                                                                                                                                                                   YVRTCIMDNGVSYRGTVARTAGGLPCQAWSRRFPNDHKYTPTPKNGLEENFCRNPDGDPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1114.5; DB Pred. No. 4.8e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F;1-77/Domain: activation peptide #status predicted <APT>
F;7-56-60/Product: plasmin chain A #status predicted <ACH>
F;84-162/Domain: kringle homology <KR1>
F;166-243/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen #status experimental <MIN>
F;461-540/Domain: kringle homology <KR5>
F;461-540/Domain: kringle homology <KR5>
F;461-540/Domain: kringle homology <KR5>
F;661-783/Domain: kringle homology <KR5>
F;661-783/Domain: kringle homology <KR5>
F;561-783/Domain: kringle
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(;Date: 07-5ep-1990 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S03733; S03737; A25834
R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kri
F;1-790/Product: plasminogen #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-57 < BRU's
R; Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
Eyr. J. Biochem. 149, 279-285
Eyr. J. B
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R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Mann Eur. J. Biochem. 114, 465-470, 1981
Eur. J. Biochem. 16, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03737
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A; Residues: 450-790 < MAR>
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    ,645,740/Active site: His,
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plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: A35514; S48202; S48203
R;Degen, S.J.F; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A;Title: Characterization of the CDNA coding for mouse plasminogen and localization of A;Reference number: A38514; MUID:91184812; PMID:2081600
A;A;Refectence number: S48514
A;Molecule type: mRNA
A;Residues: 1-812 <DEG>
A;Cross-references: UNIROT:P20918; GB:J04766; NID:9200402; PIDN:AAA50168.1; PID:920040
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Reference number: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIJ>A;Accession: S48203
A;Molecule type: protein
A;Residues: 22-27 <LI2>C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin mediately after dissociation from the clot. In the presence of the inhibitor, the activation involves also removal of the activation peptide.
C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. The string solid tumors.
C;Function:
C;Function:
C;Function: dissolves the fibrin of blood clots; acts as a proteolytic factor in a very state of the careful of 
  ns the walls of A; Pathway: fibr C; Superfamily:
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F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR2>
F;377-454/Domain: kringle homology <KR4>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;582-812/Domain: kringle homology <KR5>
F;582-812/Domain: kringle homology <KR5>
F;582-805/Domain: trypsin homology <TRY>
F;582-805/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bonds: #status predicted

F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predict

F;136,308/Binding site: carbohydrate (Asn) (covalent) #status
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Best Local
443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 TKKVNTA---DOCANRCTRNKGLPFTCKAFVFDKARKOCLWFPFNSMSSGVKKEFGHEFD
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SVRWEYCNLKRC-SETGGSVV
                                        LIPWDYCPISRCEGDTTPTIV
                                                                                                                                  GNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNP
                                                                                                                                                                             DGETAPWCYTTDSQLRWEYC-EIPSCESSASPDQSDSSVPPEEQTPVVQECYQSDGQSYR
                                                                                                                                                                                                                             DGSESPWCFTTDPNIRVGYCSQIPNCDMSHG---
                                                                                                                                                                                                                                                                            PPSPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEENYCRNP
                                                                                                                                                                                                                                                                                                    VPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCOPWSSMIPHEHSYR-----GKDLQENYC
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                                                                                                                                                                                                                                                                                                                                                                    QSPHAHGYIPAKFPSKNLKMNYCHNPDGEPRPWCFTTDPTKRWEYCDIPRCT----TPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNPDNDEQGPWCYTTDPDKRYDYCNIPECEE
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Pred. No. 1.2e-66;
4; Mismatches 144;
                                             442
                                                                                          HRHSKTPENFPDAG-LEMNYCRNPDGD
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plasmin (EC 3.4.21.7) precursor - western European hedgehog C;Species: Erinaceus europaeus (western European hedgehog) C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_cha C;Accession: 146260
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; V J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cla A;Reference number: 146259; MUID:96025778; PMID:7592597
A;Accession: 146260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

#text\_change

09-Jul-2004

cloning Wade,

of hedgehog D.P.;

apolipopro C.D.;

Byrne,

Fon

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F;103-181/Domain: k
F;185-262/Domain: k
F;275-352/Domain: k
F;377-454/Domain: k
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F;379-456/Domain: )
F;482-561/Domain: )
F;582-803/Domain: t
                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-810 < TOM>
A; Residues: 1-810 < TOM>
A; Cross-references: UNIPROT: P12545; GB: J04697; NID: g342272; PIDN: AAA36901.1; PID: g342273
C; Superfamily: plasmin; kringle homology; plasminogen-related protein nracurron c; Keywords: fibrinolysis: glucorrotain
                             F;1-96/Domain: plasminogen-related process.
F;1-9/Domain: signal sequence #status predicted
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F:375-352/Domain: kringle homology <KR3>
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B30848

C.Species: Macaca mulatta (rhesus macaque)
C.Species: Macaca mulatta (rhesus macaque)
C.pate: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change
C.Accession: B32869; B30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A.Title: Rhesus monkey apolipoprotein(a). Sequence, evolution,
A;Reference number: A32869; MUID:89174660; PMID:2925643
A;Accession: B32869
A;Status: preliminary
A,Solerylatroe.mana
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A;Cross-references: UNIPROT:Q29485; EMBL:U33171; NID:g1046360; PID:g1046361 C;Superfamily: plasmin, kringle homology; plasminogen-related protein precu: C;Keywords: hydrolase; serine proteinase F;1-96/Domain: plasminogen-related protein precursor homology <PLPH> F;103-181/Domain: kringle homology <KR1> F;185-282/Domain: kringle homology <KR2>
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192; Conserv
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                                                                                                 plasminogen-related protein precursor homology <PLPH>
signal sequence #status predicted <SIG>
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i: kringle homology <KR3>
i: kringle homology <KR4>
i: kringle homology <KR5>
i: trypsin homology <TRY>
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Pred. No. 2.2e
64; Mismatches
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                                                                                                                                                                                                                                                                                                       synthesis.
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R;Berglund, L.; Andersen, M.D.; Petersen, T.I. submitted to the EMBL Data Library, May 1994 A;Description: Cloning and characterizatin of A;Reference number: $45046 A;Accession: $45046
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F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
bonds: #status predicted
F;622,665,760/Active site: His, Asp, Ser #status predicted
A;Residues: 1-812 <BER>
A;Cross-references: UNIPROT:P06868; EMBL:X79402; NID:g494962;
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
                                                                                                                                                                                    C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence revision 28-Apr-1995
C;Accession: S45046; A25835; I45961; S03736
                                                                                                                                                                                                                                            plasmin (EC 3.4.21.7) precurson
N; Alternate names: plasminogen
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                                                              A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR-----GKDLQENYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPDGEKAPWCYTTNSQVRWEYC-KIPSCESSPVSTEPLDPTAPPELTPVVQECYHGDGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPSSGPTYQCLKGTGENYRGDVAVTVSGHTCHGWSAQTPHTHNRTPENFPCKNLDENYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPLE - - TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNPDNDGQGPWCYTTDPEERFDYCDIPEC-EDECMHCSGENYDGKISKTMSGLECQAWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFEKKVYLSECKTGNGKNYRGTMSKTRTGITCQKWSSTSPHRPTFSPATHPSEGLEENYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKKQLGAGSIEECAAKCEEEE--EFTCRSFQYHSKEQQCVIMAENRKSSIVFRM--RDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKK---VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD
                                                                                                                                                                                                                                                                                                                                                                      WCFTTDPSVRWEYCNLKKCSG
                                                                                                                                                                                                                                                                                                                                                                                                           WCYTGNPLIPWDYCPISRCEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRGTSSTTTTGKKCQSWSSMTPHWHEKTPENF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YMGNLSQTRSGLTCSMW-----DKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGP
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42.2%;
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Pred. No. 2.6e-65;
                                                                                                                                                                                                                                                                                                                                                                      456
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                                                                                                                                                                 T.E.
                                                                                                                            0f
                                                                                                                              bovine
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                                                                                                                          plasminogen
                          PIDN:CAA55939.1; PID:g4949
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A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I45961
A;Status: translated from GB/EMBL/DDBJ
A;Molecule trans

A; Molecule type: protein A; Residues: 27-334,'D', 336-515,'H',517-554,'L' R; Malinowski, D.P.; Sadler, J.E.; Davie, E.W. Biochemistry 23, 4243-4250, 1984

,556-812

coding

for

A; Reference number: A25835; A; Accession: A25835

A;Note: it is uncertain whether Met-1 or Met-8 is the initial R;Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosse. Eur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine plasminogen. A;Reference number: A25835; MUID:85203906; PMID:3846532

is the initiator G.A.K.; Rosselet,

S.J.; Kampfer,

Rick

Comparison

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A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A;Accession: S03735 MUID:81212097; PMID:7238497 A;Residues: 27-83 <BRU>
C;Function:
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F;104-183/Domain: kringle homology <KR1>
F;192-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR3>
F;282-359/Domain: kringle homology <KR3>
F;384-461/Domain: kringle homology <KR4>
F;384-461/Domain: kringle homology <KR5>
F;485-564/Domain: kringle homology <KR5>
F;584-802/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;584-805/Domain: trypsin homology <TRY>
F;564-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33
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C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor
C;Superfamily: plasmin; fibrinolysis; glycoprotein; hydrolase; kidney; kringle;
C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>
F;27-812/Product: plasminogen #status experimental <PRO>
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F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583,584-812/Product: plasmin #status experimental <APT>
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446 TTDPRVRWEFCNLKKC
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                                                                                                                                                                                                  CRNPNGEKAPMCYTTNSEVRWEYCT-IPSCESSPLSTERMDVPVPPEQTPVPQDCYHGNG
                                                                                                                                                                                                                                                        CRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH-------GQDCYRGNG
                                                                                                                                                                                                                                                                                                          TPPPSSGPKYQCLKGTGKNYGGTVAVTESGHTCQRWSEQTPHKHNRTPENFPCKNLEENY
                                                                                                                                                                                                                                                                                                                                                                                                                                             DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRFWCYTLDPHTRWEYCAIKTCADNTMND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRW
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                                                 TGNPLIPWDYCPISRC
                                                                                                     QSYRGTSSTTITGRKCQSWSSMTP--HRHLKTPENYPNAG-LTMNYCRNPDAD-KSPWCY
                                                                                                                                                   KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCY
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461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1019.5; DB 1; Length 812; Pred. No. 3.3e-65; 73; Mismatches 137; Indels 43.
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RESULT PLHU

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A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PI
A;Experimental source: liver
R;Malinowski, D.P.; Sadder, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic
A;Reference number: I45961; MUID:85023311; PMID:6148961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmin (EC 3.4.21.7) precursor [validated] - human
N;Alternate names: plasminogen precursor [misnomer]
N;Contains: angiostatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004
C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627;
C;Accession: T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-611, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme
A;Reference number: A35229; MUID:90202879; PMID:2318848
                                                                                                                                                                                                                                                                      Eur. J. Blochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin
A;Reference number: A04627, MUID:77225245; PMID:142009
A;Accession: A04627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 20-71, E', 73-76 <BRU>
R;Sottrup-densen, L: petersen, T.E.;
submitted to the Atlas, July 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Eur. J. Biochem. 114, 465-470, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 292-471, 'D', 473-810 <MAL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning and characterization of a full-length cDNA clone for human A;Reference number: A26646; MUID:87162490; PMID:3030813
A;Accession: A26646
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A;Title: Definition of the transcription initiation site of human plasminogen gene in l A;Reference number: 152242; MUID:91097523; PMID:2268308
   A; Reference number: A; Accession: A04625
                                                                                                                                    A;Molecule type: protein
A;Residues: 581-810 <WII>
R;Wiman, B; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues:
R;Wiman, B.
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A; Accession: A00929
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A; Residues: 367-419
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A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
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A; Residues: 1-471, 'D', 473-810 <FOR>
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A; Residues: 1-16 < MAL1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: K02922; NID: g190112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: I62738
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                                                                                                 Structural relationship between "glutamic acid" and
A04625
                                      A04625; MUID:75093329;
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                                      PMID: 122932
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R; de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.;

Tulinsky, A.; Westbrook,

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J. Biol. Chem. 259, 13690-13694, 1984
A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential A;Reference number: A92458; MUID:85054794; PMID:6094526
A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.; J. Biol. Chem. 271, 29461-29467, 1996
A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferativ A;Reference number: A58811; MUID:97067211; PMID:8910613
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A;Title: Studies on the active center of human plasmin. A;Reference number: A92048; MUID:69234739; PMID:4240117
A;Contents: annotation; active site
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J. Biol. Chem. 257, 7401-7406, 1982
A;Title: Structure of the omega-aminocarboxylic acid-binding sites
A;Reference number: A92382; MUID:82213905; PMID:6919539
A;Contents: annotation; omega-aminocarboxylic acid binding sites
R;Vali, Z.; Patthy, L.
J. Biol. Chem. 259, 13690-13694, 1984
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A; Residues: 483-507; E; 5.509-604 <WI3>
A; Residues: 483-507; E; 5.509-604 <WI3>
J. Biol. Chem. 248, 1631-1633, 1973
A; Title: The primary structure of human plasminogen. II.
A; Reference number: A92125; MUID:73149248; PMID:4694729
A; Contents: annotation; active site
A; Groskopf, W.R.; Summaria, L.; Robbins, K.C.
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Eur. J. Biochem. 58, 539-547, 1975
Biochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid complex of human
A;Reference number: A58818; MUID:92031503; PMID:1657149
                                                                                                                                                                                                                                   A;Contents: annotation; X-ray crystallography, 2.1 angstroms, R;Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G. Biochemistry 30, 10576-10588, 1991
A;Tille: Crystal and molecular structure of human plasminogen A;Reference number: A58819; MUID:92031502; PMID:1657148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Padmanabhan, K.; Tulinsky, A. submitted to the Brookhaven Protein Data Bank, A;Reference number: A52408; PDB:1PMK
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A;Reference number: A51341; PDB:1PK4
A;Contents: annotation; X-ray crystallography, 1.9 angstroms,
R;Tulinsky, A.; Wu, T.P.
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                                                                                                                                          Contents: annotation Wu, T.P.; Padmanabhan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contents: annotation; X-ray crystallography,
                                                                                                  10589-10594, 1991
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                                                                                                                                          K.; Tulinsky, A.; Mulichak, A.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 December 1995
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152 141

RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 201

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A; Contents: annotation; conformation by (1)H-NMR
C; Comment: plasminogen is synthesized by the kidney and is present in plasma and many ot C; Comment: plasminogen is synthesized by the kidney and is present in plasma and many ot C; Comment: plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU a d PIR:FGHUGB) in is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately af C; Comment: plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately af C; Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial cond C; Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. To
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A;Reference number: A65804; PDB:HPK
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: S43645; MUID:94237157; PMID:8181475
A;Rejante; annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                     F;97-580,581-810/Product: plasmin #status experimental F;97-580,581-810/Product: plasmin #status experimental F;97-580/Domain: plasmin chain A #status experimental F;103-181/Domain: kringle homology <KR2> F;185-262/Domain: kringle homology <KR3> F;275-352/Domain: kringle homology <KR3> F;377-454/Domain: kringle homology <KR4> F;481-560/Domain: kringle homology <KR5> F;550-580,581-810/Product: microplasmin #status experimental F;550-580,581-810/Product: microplasmin #status experimental F;97-580,581-810/Product: microplasmin #status experime
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C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: anglogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
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A; Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Contents: annotation; X R;Rejante, M.; Llinas, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue
A;Reference number: A39483; MUID:92118803; PMID:1310033
B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GDB:119498; OMIM:173350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;20-96/Domain: activation peptide #status experimental
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                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                             191;
                                                                                                                                                                                                                                                                                 Similarity
TKKQLGAGSIEECAAKCEEDE--EFTCRAFQYHSKEQQCVIMAENRKSSIIIRM--RDVV
                                                                                                            TKK---VNTADOCANRCTRNKGLPFTCKAFVFDKARKOCLWFPFNSMSSGVKKEFGHEFD
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                                                                                                                                                                                                                                                                                 39.5%;
43.1%;
                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                 Score 1018.5; DB 1; Pred. No. 3.9e-65;
                                                                                                                                                                                                                             Mismatches
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	Qy 3 Db 27	Qy 31 Db 272	Qy 2 Db 26	Qy 1 Db 26	Qy 14 Db 255	Qу Db 24	Query Match Best Local Matches 17	A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-2869 <1 A; Cross-references: U A; Experimental source C; Comment: The lipopr ent apollpoprotein(a)	R;Lawn, R.N J. Biol. Ch A;Title: Th A;Reference	RESULT 15 T18518 apolipoprot C;Species: C;Date: 15- C;Accession	Db 4	Qy 4	ОУ 3 Въ 3	Db 3	Оу з		Q <sub>Y</sub> 2	Db 2		Db 1
22 LIPWDYCPISRCEGDTTPT 440 ;  :	965 GNLSQTRSGLTCSWWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNP 421	313 LRENYCHNDDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQD-CYRGNGKNYM 364	253 ADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKD 312 :::  ::  :	193 GKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTC 252  -         -     -      -	144 PRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGIMDHTES 192	89 ENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYRGKDLQENYCRN 143	ch 35.9%; Score 927; DB 2; Length 2869; il Similarity 45.4%; Pred. No. 4.9e-58; 172; Conservative 50; Mismatches 123; Indels 34; Gaps 11;	preliminary; translated from GB/EMBL/DDBJ e type: mRNA e type: mRNA s: 1-2869 <lam> ferences: UNIPROT:Q28398; EMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AAC485 ental source: liver The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con poprotein(a).</lam>	R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong Chem. 270, 24004-24009, 1995  The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot nce number: 146259; MUID:96025778; PMID:7592597	tein(a) - western European hedgehog (fragment) Erinaceus europaeus (western Buropean hedgehog) -Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 n: T18518		20 NPLIPWDYCPISRCEGDTTPTIV 442	363 YMGNLSQTRSGLTCSMWDKNWEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTG 419 	26 NPDGKR	20 NPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRC	66 PPSSGPTYQCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCR 32	262 VPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 319		C OMBENATIONES TO THE PARTY OF THE THE TRANSPORT OF THE T	

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1: uniprot_sprot:*
2: uniprot_trembl:*
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   ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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                                           HGFL MOUSE
O91XG8
O91XG8
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PLMN RAT
PLMN MACEU
PLMN PIG
O6TCIO
PLMN MOUSE
O42341
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Q86781
Q76881
Q96H09
Q8C9G5
HGF MOUSE
HGF RAT
Q90978
Q91402
Q788Q2
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PLMN_BACMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Search time 64.6344 Seconds (without alignments) 3501.834 Million cell updates/sec
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                 Q90zn6
Q13208
P70521
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Q91x98
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O18783
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5 xenopus lae
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felis silve
mus musculu
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canis famil
   taurus
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## ALIGNMENTS

RT RX RR RT	RRRRRR	R R R R R R R R R R R R R R R R R R R	RRIT RAAR RRAAR RAAR RAAR RAAR RAAR RAAR	RESULT HGF_HU ID H AC P AC P DT 0 DT 2 DT 2 DE (() GN H GN H OC M OC M
loning and ex 40-443(1989). M N.A. (ISOFO nta; 00441; PubMed= Kitamura A., ively process r gene.";	(ISOFORM 1), AND SEQUENCE OF 55-73 AND 495-520.  PubMed=2531289; DOI=10.1038/342440a0;  Zawa T., Hagiya M., Seki T., Shimonishi M.,  Zo K., Shimiu S.;	SEQUENCE FROM N.A. (ISOFORM 1).  SEQUENCE FROM N.A. (ISOFORM 1).  TISSUE=Leukocyte;  MEDLINE=91025062; PubMed=2145836;  MEDLINE=91025062; PubMed=2145836;  MEDLINE=91025062; PubMed=2145836;  MEDLINE=91025062; PubMed=2145836;  Seki T., Ihara I., Sugimura A., Shimozu S.;  Hagiya M., Nakamura T., Shimizu S.;  "Isolation and expression of cDNA for different forms of hepatocyte growth factor from human leukocyte.";  Biochem. Biophys. Res. Commun. 172:321-327(1990).	SEQUENCE FROM N.A. (ISOFORM 1).  SEQUENCE FROM N.A. (ISOFORM 1).  SEQUENCE FROM N.A. (ISOFORM 1).  Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;  Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;  Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;  Seci T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;  "Organization of the human hepatocyte growth factor-encoding gene.";  Gene 102:213-219(1991).  [2]  SEQUENCE FROM N.A. (ISOFORM 1).  TISSUE=Placenta;  MEDLINE=89392017; PubMed=2528952;  Miyazawa K., Teubouchi H., Naka D., Takahashi K., Okigaki M., Arakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,  Gohda E., Daikuhara Y., Kitamura N.;  "Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factor.";  Biochem. Biophys. Res. Commun. 163:967-973(1989).	HUMAN  HUMAN  STANDARD;  PRT;  728 AA.  P14210; Q02935; Q13494; Q14519; Q8FCE2; Q9BYL9; Q9BYM0; Q9UDU6;  01-JAN-1990 (Rel. 13, Created)  01-AUG-1991 (Rel. 19, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Hepatocyte growth factor precursor (Scatter factor) (SF) (Hepatopoeitin A).  Name=HGF; Synonyms=HPTA; Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;

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MEDLINE-2737999; PubMed=12853948; DOI=10.1038/nature01782;
A Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
Wagner-McPherson C., Layman D., Maass J., Jaeger S., Walker R.,
A Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
A Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
A Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
A Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M.,
A Coersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
A Coersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
A Coersky P., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
A Colowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
A Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
A Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
A Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
A Mendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
A Mendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
A Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Bubb K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Minimum County of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A functional domain in the heavy chain growth factor binds the c-Met receptor abut not mitogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LYS-304 AND TYR-330. Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; "NIEHS S15478, Department "NIEHS-SNPs, environmental genome project, NIEHS E315478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93087571; PubMed=1280830; MEDLINE=93087571; PubMed=1280830; Meidner K.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a competitive HGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evidence for the identity of human scatter factor
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P.M., Birch
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Hirschfield D.W.,
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., Bottaro D.P., Taylor W.G.,
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Hishida T., Daik
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOShiyama Y., Arakaki N., Naka D., Nakayama H., Gohda E., Kitamura N., Hishida T., Daikuhara Y.;
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Baertsch R.A., Brent M.R., K
Bailey J.A., Portnoy M.E., T
Eddy S.R., McPherson J.D., O
Waterston R.H., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyazawa K., Kitamura A., Kitamura N.; "Structural organization and the transcription human hepatocyte growth factor gene."; Biochemistry 30:9170-9176(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The DNA sequence of human chromosome Nature 424:157-164(2003).
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EMBO
                                                                                                                                                                                                                                            Lokker N.A., Mark M.R
Baker J.B., Godowski
                                                                                                                                                                                                                                                                                                                                                    "Hepatocyte growth factor is linked on the alpha chain.";
                                                                                                                                                                                                                                                                                                                                                                                   Shimizu N., Hara H., Sogabe T.,
Nakamura T., Shimizu S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITE THR-476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hishida T., Daikunara 1.;
"Identification of the N-terminal residue of the heavy
"The state of the N-terminal residue of the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91369928;
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                                                                                                     Zhou
                                                                                                                                                                                                                                                                                 MEDLINE=92331602;
                                                                                                                                                                                                                                                                                                 MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                    Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93129192;
                                                                                     Rubin J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            [16]
                                                                                                                      MEDLINE=98154323;
                                                                                                                                                                                                          Structure-function analysis of hepatocyte growth factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse cDNA sequences.
                           INB=98154323; PubMed=9493272; DOI=10.1016/S05
H., Mazzulla M.J., Kaufman J.D., Stahl S.J.,
n J.S., Bottaro D.P., Byrd R.A.;
solution structure of the N-terminal domain
or reveals a potential heparin-binding site."
cture 6:109-116(1998).
                                                                                                                                                                         affinity receptor binding.";
J. 11:2503-2510(1992).
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                                                                                                                                                                                                                                                                                                                                  Biophys.
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wski P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . (ISOFORMS 5 AND 6).
PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                              PubMed=1321034;
M.R., Luis E.A.,
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D., Stahl S.J., Wingfield P.T.,
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, Tsubouchi H., Ishii
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05-JUL-2004
                                                                                SEQUENCE FROM N.A.
Liao A.T., Chien M.B., London C.A.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ
--- SIMILARTY: Belongs to peptidase family S1
EMBL; AB090353; BAC57560.1; --
EMBL; AY543632; AAS48570.1; --
EMBL; AY543632; AAS48570.1; --
EMBL; P14210; IGMN.
                                                                                                                                                                                                                                                                                                              MEDLINE=22844761; PubMed=12963274; DOI=10.1016/S0165-2427(03)00118-1; Miyake M., Saze K., Yaguchi T., Wang J., Suzuta Y., Haga Y., Takahashi S.Y., Yamamoto Y., Iwabuni S.; "Canine hepatocyte growth factor: molecular cloning and characterization of the recombinant protein."; Vet. Immunol. Immunopathol. 95:135-143(2003).
MEROPS; S01.982;
GO; GO:0004263; 1
GO; GO:0008233; 1
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Best Local S
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GO, GO:0006508; P:proteolysis and peptidolysis; IE;
InterPro; IPR011359; HGF_MST1.
InterPro; IPR001001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003014; PAN.
InterPro; IPR003019; Pan app.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; pP00024; PAN; 1.
Pfam; PP00089; Trypsin; 1.
Pfam; PP00089; Trypsin; 1.
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PERMI, PROCOST, TRYPSIN; 1.
PRINTS; PROOTS; CHYMOTRYPSIN.
PRINTS; PROOTS; KRINGLE.
PROODOM; PROOTS; KRINGLE.
PRODOM; PROOTS; KRINGLE.
1.
SMART; SMOO130; KR; 4.
SMART; SMOO130; TRYPSPC; 1.
PROSITE; PSOO021; KRINGLE 1; 4.
PROSITE; PSOO701; KRINGLE 2; 4.
PROSITE; PSOO701; KRINGLE 3; 4.
PROSITE; PSOO
                                                                                Q76BS1;
Q76BS1;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                          Hepatocyte Name=hgf;
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     taurus
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                                                                                                                                                                                                                                                                                                                                                                                  CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRGNGKNYMGNLSKTRSGLTCSMWEKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
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4 (TrEMBLrel. 2
growth factor.
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91.9%;
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Pred. No. 6.5e
19; Mismatches
                                                                                                                                               Created)
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4E83F9EA8BFF6DB1
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.5e-175;
.es 12;
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                                                                                         update)
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211

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Query Match
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Matches 409
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RMBL AB110822; BAD02475.1; -.

RSSP; P08519; IKIV.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; P:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; II
InterPro; IPR001359; HGF MST1.
InterPro; IPR003001; Kringle.
InterPro; IPR003509; Pan_app.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Piptidase_S1A.
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PRINTS; PRO0018; KRINGLE.
PRODOM; PD000395; KRINGLE;
PRODOM; PD000395; KRINGLE;
SMART; SM00110; KR; 4.
SMART; SM00020; TRYP_SPC; 1.
SMART; SM00020; TRYP_SPC; 1.
SMART; PS00021; KRINGLE 1; 4.
PROSITE; PS50070; KRINGLE 2; 4.
PROSITE; PS50048; PAN; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
HYDROSITE; PS50240; TRYPSIN_DOM; 1.
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Bovinae; Bos.
NCBI_TaxID=9913;
[1]
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Pfam; PF00024; PAN; 1.
Pfam; PF00089; Trypsin;
PIRSF; PIRSF001152; HGF
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CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                                                      YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
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                                                                                         YRGNGKNYMGSLSKTRSGLTCSMWDKNMEDLHRHIFWEPDATKLNKNYCRNPDDDAHGPW
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83357 MW; E39D65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.8%;
91.5%;
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Pred. No. 1.8e
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E39D653B0A85F49B CRC64;
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databases.
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Best Local S
Matches 409
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GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IE

InterPro; IPR001359; HGF MST1.

R InterPro; IPR003014; PAN.

R InterPro; IPR003014; PAN.

R InterPro; IPR00314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.
                                                                                                                                                                       PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0018; KRINGLE.
PRODOM; PD000195; Kringle; 4.
SMART; SM00110; KR; 4.
SMART; SM00110; KR; 4.
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; TRYBESI 1.
PROSITE; PS00070; KRINGLE 1; 4.
PROSITE; PS50070; KRINGLE 2; 4.
PROSITE; PS50070; TRYPSIN_DOM; 1.
PROSITE; PS50248; PAN; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Kringle; Protease; Sesequence 728 AA; 83067 MW; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
Kobayashi Y.,
Tsujimoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haga Y., Yamamoto Y., Takahashi S., J
Submitled (FEB-2002) to the EMBL/GenE
-:- SIMILARITY: Belongs to peptidase
EMBL; AB0446610; BAB21499.1; -.
EMBL; AB080187; BAC10545.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BH09;
Q9BH09;
                                                                                                                                                                                                                                                                                                                        Pfam; PF00051; Kringle; 4.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001152; HGF_MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyake M., Yaguchi
Haga Y., Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB080187; BAC:
HSSP; P14210; 1GMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatocyte
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                                                                                                                           409;
                                                 61
                                                                         30
                                                                                                                                      Similarity
                                                                        CYTGNPLIPWDYCPISRCEGDTTPTIV
 WSSMI PHEH - - -
                                      ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                         ARKRCLWFPFNSMTSGVKKEFGHEFDLY
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                                                                                                                           Conservative
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                                                                                                                                                                          Protease; Serine protease.
83067 MW; 8D7F4A333D1E190A CRC64;
                                                                                                                                      93.6%;
91.5%;
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Takahashi
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 -SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
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Last
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ashi S., Iwabuchi S.,
EMBL/GenBank/DDBJ databases
                                                                                                                         Score 2414.5;
Pred. No. 3.7e-
21; Mismatches
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es 12;
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                                                                STRAIN=C57BL/6J; TISSUB=Thymus;
MEDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDN
prepare full-length cDNA libraries for rapid discovery of
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Thymus;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome be 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
[3]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8C9G5;
01-MAR-2003
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ional annotation of a full-length 409:685-690(2001).
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Rodentia;
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOI=10.1038/35055500;
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based o
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thi; Muridae;
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                                                                                                                                                                                                                                                                                                                                           hase I & II
| functional
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; Murinae; Mus
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C STRAIN=C57BL/6J; TISSUE=Thymus;

A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci A. Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W., A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., A Hayashida K., Hayatsu N., Hiramoto K., Hiramota T., Kouda M., Koya Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya A. Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., A Sasaki D., Shibata K., Sakai C., Sakai K., Sakazume N., Sano H., A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T., Tamaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0018; KRINGLE.
PRODOM; PD000195; KRINGLE; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00020; TTYP_SPC; 1.
SMART; SM00020; TTYP_SPC; 1.
PROSITE; PS00021; KRINGLE 1; 4.
PROSITE; PS50070; KRINGLE 2; 4.
PROSITE; PS50070; KRINGLE 2; 4.
PROSITE; PS50040; TRYPSIN_DOM; 1
Hydrolase; Kringle; Processe; Se; SCITCHOP 728 A. CORON WALL
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GO; GO:0008283; P:cell proliferation; IDA.
GO; GO:0000902; P:cellular morphogenesis;
InterPro; IPR011359; HGF MST1.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
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Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001152; HGF MST1;
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InterPro;
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EMBL; AK042121; BAC31175.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>6</u>
     176
                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                               402;
                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00051; Kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P14210;
                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                  33
                                                                                                                                                                                                                                                                                                                                       Н
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                             ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                                                                                                                                     ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                                        WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                        WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                                                                                        SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCOP
                                                                                                                                                                                                                                                                                     QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003609; Pan app.
IPR001254; Peptidase_S1.
IPR001314; Peptidase_S1A.
IPR00303; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1GMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease;
82990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%;
89.9%;
                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease.
8D5258DF3BCF3545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2371.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                .6e-171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kamura M.,
Okazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci
                                                                                                                                                                                                                                                                                                                                                                                                                                                        728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koya
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Ś В Ş g δ 뮍 á

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RESULT 6
HGF_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Mammary fibroblast;
MEDLINE=94183257; PubMed=8135822;
Sasaki M., Nishio M., Sasaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGF_MOUSE STANDARD; PRT; 728 AA. 080348; Q61662; Q64007; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                           hepatocyte growth factor.",
Biochim. Biophys. Acta 1216:299-303(1993).

-!- FUNCTION: HGF is a potent mitogen for mature parenchymal hepatocyte cells, seems to be an hepatotrophic factor, are growth factor for a broad spectrum of tissues and cell ty has no detectable protesse activity.

-!- SUBUNIT: Dimer of an alpha chain and a beta chain linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94363381; PubMed=8081873;
Lee C.C., Kozak C.A., Yamada K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki M., Nishio M., Sasaki T., Enami J.;
"Identification of mouse mammary fibroblast-derived factor as hepatocyte growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatocyte growth factor precursor (Hepatopoeitin A).
  <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94060105; PubMed=8241272; DOI=10.1016/0167-4781(93)90159-B;
Liu Y., Michalopoulos G.K., Zarnegar R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee C.C., Kozak C.A., Yamada K.M.;
"Structure, genetic mapping, and expression of the mouse Hgf/scatter teator gene.":
                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and characterization of cDNA encoding
nepatocyte growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                        IsoId=Q08048-2; Se
SIMILARITY: Belongs
                                                                                     Name=Short
                                                                                                                               Name=Long;
                                                                                                                                                 Event=Alternative
                                                                                                                                                                          ALTERNATIVE PRODUCTS:
                                                                                                                                                                                            disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
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                                                                                                         IsoId=Q08048-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPN1RVGYCSQ1PNCDMSHGQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTLDPDTTWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Commun. 1:101-111(1993).
  Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Res. Commun. 199:772-779(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORMS
                                        Sequence=VSP_005408;
gs to the peptidase S
                                                                                                       Sequence=Displayed;
                                                                                                                                                 splicing;
4 kringle domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Veri
Sciurognathi;
                                                                                                                                                 Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND SHORT),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Scatter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                            Sı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor)
                                          family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 496-504
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                                            Plasminogen
                                                                                                                                                                                                                linked by
                                                                                                                                                                                                                                                                                                                                                                    mouse
                                                                                                                                                                                                                                                          and acts
types. It
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STITE STATE OF THE STATE OF THE
Query Match
Best Local S
Matches 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00051; Kringle; 4.
Pfam; PF00084; PAN; 1.
Pfam; PF00089; Trypsin; 1.
PIRSP; PIRSP001152; HGF MST1; 1.
PRINTS; PR007182; KGYMOTRYPSIN.
PRINTS; PR007182; KRINGLE.
PRODOM; PR000395; KRINGLE.
PRODOM; PR000395; KRINGLE.
SMART; SM000473; PAN AP; 1.
SMART; SM00473; PAN AP; 1.
SMART; SM00473; PAN AP; 1.
PROSITE; PS0070; KRINGLE 2; 4.
PROSITE; PS50070; KRINGLE 2; 4.
PROSITE; PS50948; PAN; 1.
PROSITE; PS50948; PAN; 1.
PROSITE; PS50948; PAN; 1.
                                                                                    CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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DISULFID
CARBOHYD
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CARBOHYD
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MOD_RES
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DOMAIN
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SIGNAL
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EMBL; D10213; BAA01065.1; -.
EMBL; S71816; AAB31855.1; -.
EMBL; X72307; CAA5154.1; ALT_INIT.
EMBL; X72307; CAA5154.1; ALT_INIT.
EMBL; X72307; CAA5185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003609; Pan app.
InterPro; IPR009003; Pept Ser_Cys.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing; Direct protein sequencing; Glycoprotein; Growth factor; Kringle; Pyrrolidone carboxylic acid; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:96079; Hgf.
GO; GO:00008283; P:cell proliferation; IDA.
GO; GO:0000902; P:cellular morphogenesis;
                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P14210; 1BHT.
                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS;

    !- SIMILARITY: Contains 1 PAN domain.

    402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease
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                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001314; Peptidase_S1A
                                                                                  564
728
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392
496
71
    Conservative
                                                                                                                                                                                                                    488
295
403
569
656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homolog;
32
495
728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN_DOM; 1.
                                                                                       344 N
479 V
564 R
82944 MW;
                                                                                                                                                                                             124
207
289
384
470
728
97
728
607
295
403
569
656
                        91.9%;
89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
    21;
                                                                                                        Missing (in isoform )
/FTId=VSP 005408.
N -> K (in Ref. 2).
V -> L (in Ref. 2).
R -> H (in Ref. 3).
  Score 2370.5;
Pred. No. 7.8e
?1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Kringle 1.
Kringle 2.
Kringle 3.
                                                                                                                                                                                                               Interchain (By similarity).

W-linked (GlCNAc. . ) (Potential).

N-linked (GlCNAc. . ) (Potential).

N-linked (GlCNAc. . ) (Potential).

N-linked (GlCNAc. . ) (Potential).
                                                                                       V -> L (in Ref. 2).
R -> H (in Ref. 3).
; A0381FC497534328 CRC64;
                                                                                                                                                                                                                                                                                                                          Serine protease-like
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatocyte growth factor alpha chain. Hepatocyte growth factor beta chain. Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
                                                                                                                                                                                                                                                                                                                                                                                           Kringle 4.
                          .8e-171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDA.
                                            DB
                                            <u>ب</u>
                                                                                                                                                                                               Short).
    Indels
                                            Length
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      Gaps
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RESULT 7
HGF RAT
ID - HGF
AC -
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                                                      SEQUENCE FROM N.A.

C STRAIN=Wistar; TISSUE=Liver;

X MEDLINE=91031482; PubMed=2146117;

X MEDLINE=91031482; PubMed=2146117;

A Okajima A., Miyazawa K., Kitamura N.;

Its mRNA during liver regeneration following hepatic injury.";

L Eur. J. Biochem. 193:375-381(1990).

C -!- FUNCTION: HGF is a potent mitogen for mature parenchymal hepatocyte cells, seems to be an hepatotrophic factor, and a growth factor for a broad spectrum of tissues and cell types of the seems no detectable protease activity.

C -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by disulfade bond.

C -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                            HGF_RAT STANDARD; PRT; 728 AA. P17945; O1-NOV-1990 (Rel. 16, Created) O1-NOV-1990 (Rel. 16, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Hepatocyte growth factor precursor (Scatter f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Wistar; TISSUE=Liver;
MEDLINE=90222197; PubMed=2139229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Hepatopoeitin A).
  subfamily.
SIMILARITY:
SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     norvegicus (Rat).
ota; Metazoa; Chordata;
ia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTGNPLIPWDYCPISRCEGDTTPTIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
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    Contains
                         Contains
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    kringle domains PAN domain.
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87:3200-3204(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Veri
Sciurognathi;
                                                                                                            activity.
chain and a beta chain linked by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth
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                                                                    Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor
                                                                                                                                                                                                                                               injury.";
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                                                                                                                                                                                                                                                                       induction
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                                                                                                                                                                               Query Match
Best Local S
Matches 399
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00089; Trypsin; 1.

PRINTS; PTRSF001152; HGF MST1; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00128; KRINGLE.

ProDom; PD000395; Kringle; 4.

SMART; SM00100; KR; 4.

SMART; SM00100; Tryp SPC; 1.

SMART; SM00173; PAN AP; 1.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00071; KRINGLE 1; 4.

PROSITE; PS00071; KRINGLE 2; 4.

PROSITE; PS50070; KRINGLE 2; 4.
                                                                                                                                                                                         DOMAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                               CHAIN
CHAIN
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EMBL; X54400; CAA38266.1;
PIR; A35644; A35644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through, between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00051;
Pfam; PF00024;
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGD; 2794; Hgf.
InterPro; IPR000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P14210; 1BHT
                                93
                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o; IPR003014; PAN.
j; IPR003609; Pan app.
j; IPR003003; Pept Ser Cys.
j; IPR001254; PeptIdase S1.
j; IPR001314; PeptIdase S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S01.978; -.
                                                                                                                                          Similarity
        WSSMI PHEH - - - -
                                            ARKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                               ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGS
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496
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129
212
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403
569
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82905
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728
33
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207
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384
470
728
97
85
607
295
569
                                                                                                                                           91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kringle.
-SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
                                                                                                                                                                                                                                                                                                                                                                                                                   ing; Glycoprotein; Growth factor; Kringle;
acid; Repeat; Serine protease homolog; Signal.
                                                                                                                                                                                W.
                                                                                                                              23;
                                                                                                                              Score 2363.5; DB 1;
Pred. No. 2.6e-170;
3; Mismatches 20;
                                                                                                                                                                                         Interchain (By similarity).
N-linked (GlCNAC. . .) (Pott
                                                                                                                                                                                                                                                                                        Kringle 1.
Kringle 2.
Kringle 3.
Kringle 4.
                                                                                                                                                                                                                                                   serine protease-like.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                 Hepatocyte growth factor alpha Hepatocyte growth factor beta con Pyrrolidone carboxylic acid (By
                                                                                                                                                                               N-linked (GlcNAc. . .) (
N-linked (GlcNAc. . . ) (
N-linked (GlcNAc. . . ) (
N-linked (GlcNAc. . . ) (
3EOBF1F96ADCEDFF CRC64
                                                                                                                                                                                                                                                                                                                                                       similarity).
                                                                                                                                                                                                                                                                                                                                                                                                        similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease
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                                                                                                                                                                                                                                                                                                                                                                                           factor alpha chain.
                                                                                                                                                                                CRC64;
                                                                                                                                 Indels
                                                                                                                                                       Length
                                                                                                                                                                                                        (Potential). (Potential). (Potential).
                                                                                                                                                                                            (Potential)
                                 YKGTVSITKSGIKCOP
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L outstation -
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                                                                                                                                Gaps
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WNSMI PHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDI PQCSEVEC

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357 329 297 269 237 209

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                                                        Query Match
Best Local S
Matches 336
                                                                                                                         HSSP, P14210; IGMN.

GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysi
Pfam; pF00021; Kringle; 4.
Pfam; pF00021; Kringle; 1.
Pfam; pF000089; Trypsin; 1.
PFAM; PF000089; Trypsin; 1.
PRINTS; PR00712; CHYMOTRYPSIN.
RPINTS; PR00712; CHYMOTRYPSIN.
RPINTS; PR00018; KRINGLE.
PRODOM; PD000395; Kringle; 4.
RMART; SM00130; KR; 4.
RSMART; SM001020; Tryp SPC; 1.
RPOSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50948; PAN; 1.
RPROSITE; PS50948; PAN; 1.
RROSITE; PS50948; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q90978 PRELIMINARY;
Q90978; Q90866;
01-JAN-1998 (TreMBLrel. 0
01-JAN-1998 (TreMBLrel. 0
01-MAR-2004 (TreMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=96029010; PubMed=7554499;
Thery C. Sharpe M.J., Batley S.J.,
"Expression of HGF/SF, HGF1/MSP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatocyte growth
Name=HGF/SF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ing early chick development.";
Genet. 17:90-101(1995).
SIMILARITY: Belongs to peptida
L; X84045; CAA58864.1; -.
; I11285; I51285.
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CYTGNPLVPWDYCPISRCEGDTTPTIV
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 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR
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                                                        78.1 ilarity 75.5 Conservative
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Last annotation updat
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                                                        Score 2014.5;
Pred. No. 6.5e
9; Mismatches
                                                                                                                               Serine protease.
5BD06CFB5C40B003 CRC64;
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; Galliformes; Phasianidae; Phasianinae;
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                                                        5; DB 2;
.5e-144;
les 53;
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Mech. Dev. 49:123-131(1995).

-!- SIMILARITY: Belongs to peptidase famil EMBL; S77422; ABB34554.2; -.

HSSP; P14210; 1GMN.

MEROPS; S01.976; -.

G0; G0:0004263; F:chymotrypsin activity; IEA.
G0; G0:0004295; F:trypsin activity; IEA.
G0; G0:0006203; F:protecolysis and peptidol pfam; PF00051; Kringle; 4.

Pfam; PF00051; Kringle; 4.

Pfam; PF00024; PAN; 1.

Pfam; PF00072; CHYMOTRYPSIN.
PRINTS; PR000152; HGF MST1; 1.

PRINTS; PR00018; KRINGLE.
ProDom; PF000395; Kringle; 4.

SMART; SM00130; KR; 4.

SMART; SM00130; KR; 4.

SMART; SM00020; TTYP_SPC; 1.

SMART; SM00020; TTYP_SPC; 1.

SMART; SM00020; TTYP_SPC; 1.

SMART; SM00020; TTYP_SPC; 1.

SMART; SM00020; TTYP_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
Amphibia; E
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95267690; PubMed=7748783; Nakamura H., Tashiro K., Nakamura "Molecular cloning of Xenopus HGF Xenopus early embryogenesis."; Mech Dev. 49:123-131(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatocyte
Name=HGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue=Tailbud;
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Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; I; Anura; Mesobatrachia; Pipoidea;
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T., Shiokawa K.; cDNA and its expression studies
                                                                                                                                                                                                                          peptidolysis;
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Best Local S
Matches 301
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Q788Q2;
05-JUL-2004
05-JUL-2004
                   Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
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PROSITE; PS50240; TRYPSIN
Hydrolase; Kringle; Protea
SEQUENCE 710 AA; 81487
                                                                           "A role for HGF/SF in neural induction node during gastrulation."; Development 121:813-824(1995). EMBL; X80131; CAA56430.1; -. HSSP; P00747; IKIO. InterPro; IPR000001; Kringle. InterPro; IPR000014; PAN.
                                                                                                                                                                                                        Streit A., Stern C.D., The
Sharpe M.J., Gherardi E.;
"A role for HGF/SF in neu
                     InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan app.
Pfam; PF00051; Kringle; 4.
Pfam; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGF/SF protein
Name=HGF/SF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004
HGF/SF prote
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                     MEDLINE=95237013; PubMed=7720585;
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGNPLIPWDYCPISRCEGDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMI PHEHSFLPSTYRGKDLKENYCRNPKGEEGGPWCFTKSPEVRHDVCDI PFCSEVDCVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMIPHEHS----YRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT
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27, Last sequence update)
27, Last annotation updat
27(Fragment).
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Pred. No. 5.6e
53; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
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5FE6480BE31C27FC
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Best Local S
Matches 284
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PROSITE; PS00021; KRINGLE 2; 3.
PROSITE; PS50070; KRINGLE 2; 3.
PROSITE; PS50948; PAN; 1.
Kringle; Signal.
SIGNAL
3°
SIGNAL
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                                                                                                                                                                                                                                                               Q6GP14;
05-JUL-2004
05-JUL-2004
05-JUL-2004
LOC397993 pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom;
SMART; S
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brands S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy Bosak S.A., McEwan P.J., McKernan K.J., Mahek J.A., Gunaratne P. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villakon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                    LOC397993 protein. Name=LOC397993;
                                                                                                                                                                                                                                                                                                                               Q6GP14
                                                                                                                                                     TISSUE=Spleen;
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                   Amphibia; Batrachia; Xenopodinae; Xenopus
                                                                                                                                                                                      NCBI_TaxID=8355;
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SM00473; PAN
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No. 8.
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Best Local Sim
Matches 205;
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Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDI
EMBL; BC073334; AAH73334.1; -.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007596; P:blood coagulation; IEA.
GO; GO:0007596; P:blood coagulation; IEA.
GO; GO:0007596; P:proteolysis and peptidoly.
InterPro; IPR00301; Kringle
InterPro; IPR003014; PAN.
InterPro; IPR003014; PAN.
InterPro; IPR003096; Pan_app.
InterPro; IPR003096; Pan_app.
InterPro; IPR003096; Pan_ipp:
Pfam; PF00051; Kringle; 4.

Pfam; PF00054; PAN; 1.
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PRINTS; PRO1105; PROTHOOMSIN.
ProDom; PD000395; Kringle; 4.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN AP; 1.
PROSITE; PS00021; KRINGLE 1; 4.
PROSITE; PS00070; KRINGLE 2; 4.
PROSITE; PS50948; PAN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22341132; PubMed=12454917; Klein S.L., Strausberg R.L., Wagner Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                   242
                                                                                                                                                              196
                                                                                                                                                                                                       182
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                                                                                                                                                                                                                                             FPHDHKFSPIHMPDLEENYCRNPDSDPEGPWCYTTDKNIRHQYCGIKKCEDAVCLTCNGE
                                                                                                                                                                                                                                                                     IPHEHSY---RGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE
                                                                                                                                                                                                                                                                                                                                                                 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM
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RFLPEKYPCKGLDENYCRNPDGSEAPWCFTTLPGMRMAYCFQIKRCKDDVLEPDCYHGNG
                       DMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNG
                                                                             VEKEFCRITKCKKQRLSNIEI--
                                                                                                  TRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEH
                                                                                                                                                            DYRGSVDRTESGKECQRWDLQTPHAHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTDPN
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to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Mismatches
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                                                                             -TSTCFKERGEGYRGKANTTTSGIPCQRWDSQTPQSH
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C L., Pontius J., Clifton
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Q91691
ID Q9169
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Best Local S
Matches 205
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Q91691;
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SMART; SM00130; KR; 4.
SMART; SM00473; PAN AP; 1.
SMART; SM00020; Tryp_SPc; 1.
SMART; SM000201; KRINGLE 1; 4.
PROSITE: PS50070; KRINGLE 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008239; F:thrombin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007596; P:blood coagulation; IEA.
GO; GO:000598; P:proteolysis and peptidolysis;
GO; GO:000518; Kringle; 4.
Pfam; PF00081; Kringle; 4.
Pfam; PF00081; Trypsin; 1.
Pfam; PF00081; Trypsin; 1.
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Hydrolase;
SEQUENCE
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Ruiz i Altaba A., Thery C.;
Submitted (MAY 1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN
ProDom; PD000395; Kringle; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00018; KRINGLE. PRINTS; PR01505; PROTHROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U57455; AAB52574.1; HSSP; P00746; 1FDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00021;
PROSITE; PS50070;
PROSITE; PS50948;
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                       SYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPH
                                                                                                                               IPHEHSY---RGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE
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DYRGSVDRTESGKECQRWDLQTPHAHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTDPN
                                                                                                                                                                                  CRLLPWTQNSANVLLQRNVQYDLYQKKDYIRDCVAGNGNTYRGTVSKTKSGRTCQRWRLK
                                                                                                                                                                                                                               CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCOPWSSM
                                                                                                                                                                                                                                                                         RSALNDYQRSKGLELVHMNNG-GVKQEIQSEIQVCAKQCSD----LLDCRSFVYNWKSQT
                                                                                                                                                                                                                                                                                                                    RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ
                                                                                           FPHDHKFSPIHWPELEENYCRNPDSDPEGPWCYTTDKNIRHQYCGIKKCEDAVCLTCNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kringle; Protease; Serine protease.
716 AA; 81971 MW; 508376A0E4398798 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Conservative
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, Last sequence up
, Last annotation 
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Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                Score 1198.5; DB 2;
Pred. No. 3.2e-82;
5; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and peptidolysis;
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                                                                                                                                                                                       Query Match
Best Local S
Matches 202
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GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysi
Pfam; PF00021; Kringle; 4.
Pfam; PF00025; PAN; 1.
Pfam; PF00029; Trypsin; 1.
PINSF; PR00072; CHYMOTRYPSIN.
PRINTS; PR00072; CHYMOTRYPSIN.
PRINTS; PR00011; KRINGLE.
PRODOM; PD000395; Kringle; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM001020; Tryp SPC; 1.
SMART; SM001020; Tryp SPC; 1.
PROSITE; PS000021; KRINGLE 1; 4.
PROSITE; PS000021; KRINGLE 2; 4.
PROSITE; PS50070; FRIDSEN DOM; 1.
PROSITE; PS50070; FRIDSEN DOM; 1.
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Hepatocyte growth factor-1180, mane=HGF1/MSP;
Name=HGF1/MSP;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Crances aves; Neognathae; Grances aves; Neognathae; Neognathae; Grances aves; Neognathae; Neognathae; Grances aves; Neognathae; Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96029010; PubMed=7554499; Thery C., Sharpe M.J., Batley S.J., "Expression of HGF/SF, HGF1/MSP and
                                                                                                                                                                                                                                                                                                                                         Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996
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enet. 17:90-101(1995).
                                                                                                                              ທ
                                                                                                                                                                                                                    Similarity
                                                                                                                        RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ
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      CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM
                                                               RSPLNDFQRLRGTELRAAPNEPPPSAPAHGAAQQCAQRCANRP----DCRAFHHERQSQL
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                                                                                                                                                                                                                                                                                                            Kringle; Protease; 704 AA; 79341 MW;
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llarity 45.1%; P
Conservative 72;
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BLrel. 01, Last sequence update)
BLrel. 26, Last annotation update)
factor-like/macrophage stimulating
                                                                                                                                                                                       Score 1184; DI
Pred. No. 3.9e
72; Mismatches
                                                                                                                                                                                                                                                                                                            Serine protease. CAB0D8CC41367C37
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RESULT 14
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                                                                                                                                                                                       Skeel A., Yos
Leonard E.J.;
                                                                                                                                                                                                                                                                             602-611, AND S
TISSUE=Plasma;
                                                                                                                                                                                                                                                   PubMed=1827141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
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                                                                                                                                                                                                                    Yoshimura
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HGFL HUMAN STANDARD; PRT; 711 AA.
P26927; Q13350; Q14870;
01-AUG-1992 (Rel. 23, Created)
101-AUG-1992 (Rel. 23, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hepatocyte growth factor-like protein precursor (Mastimulatory protein) (MSP) (Macrophage stimulating Name-MST1; Synonyms-HGFL;
MEDLINE=93340141; PubMed=8393443; Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.; Yoshimura T., Sequencing, and expression of human macrophage stimulating protein (MSP, MST1) confirms MSP as a member of the family of kringle proteins and locates the MSP gene on chromosome 3."; J. Biol. Chem. 268:15461-15468(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92002016; PubMed=1655021;
Han S., Stuart L.A., Friezner Degen S.J.;
"Characterization of the DNF1582 locus on
identification of a gene coding for four to hapatocyte growth factor.";
Biochemistry 30:9768-9780(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                    "Macrophage stimulating protein: p sequence, and cellular activity.";
                                                                                                                                                                                                                                               SEQUENCE OF 230-247;
602-611, AND SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPHEHSY---RGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE
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InterPro; IPRO00001; Kringle.
InterPro; IPRO030014; PAN.
InterPro; IPRO03609; Pan_app.
InterPro; IPRO03609; Pan_app.
InterPro; IPRO03030; Pept Ser Cys.
InterPro; IPRO01254; Peptidase_S1.
InterPro; IPRO01314; Peptidase_S1A.
InterPro; IPRO01314; Peptidase_S1A.
InterPro; IPRO01314; Peptidase_S1A.
InterPro; IPRO01314; Peptidase_S1A.
InterPro; IPRO01316; Peptidase_S1A.
InterPro; IPRO01316; A.
InterPro; IPRO0051; Kringle; 4.
Pfam; PF00084; PAN; 1.
Pfam; PF00084; FAN; 1.
PFRINTS; PRO01152; HGF MST1; 1.
PRINTS; PR001152; HGF MST1; 1.
PRINTS; PR001215; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
PRODOm; PD000395; Kringle; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00130; Tryp_SPC; 1.
PROSITE; PS000021; KRINGLE 1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L11924; AAA59872.1; -
PIR; A40331; A47136.
HSSP; P00766; 1CHG.
MEROPS; S01.975; -
Genew; HGNC:7380; MST1.
MIM; 142408; -
DOMAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                       Repeat;
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                   Direct protein
                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50070; KRINGLE 2; 4.
PROSITE; PS50948; PAN; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M74178;
EMBL; U37055;
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PTM: May b
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SIMILARITY: Contains 4 kringle dom
SIMILARITY: Contains 1 PAN domain.
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Dimer
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; PAN AP; 1.
; TXYD_SPC; 1.
)21; KRINGLE 1; 4.
)70; KRINGLE_2; 4.
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AAC50471.1; -.
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1105
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3355
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                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Kringle; molog; Signal.
        Kringle 1.
Kringle 2.
Kringle 3.
Kringle 4.
Serine protease-like.
By similarity.
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There are no restrictions
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Best Local Sim
Matches 196;
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PRELIMINARY; PRT; 717 AA.

P70006;
P70006;
P101-FEB-1997 (TrEMBLrel. 02, Created)
P101-FEB-1997 (TrEMBLrel. 02, Last sequence update)
P101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hepatocyte growth factor-like protein precursor.
S Xenopus laevis (African clawed frog).
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
C Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
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DISULFID
DISULFID
DISULFID
CARBOHYD
             SEQUENCE FROM N.A.
TISSUE=Kidney, and Liver;
MEDLINE=96404125; PubMed=8808403;
MEDLINES-96404125; Richter K.
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                                                                                                               Xenopodinae;
 Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR---GKDLQENYCRNPRGEEG
                                                                                                                                                                                                                                                                                                                                          FTFTSEPHAQLEENFCRNPDGDSHGPWCYTMDPRTPFDYCALRRCADDQPPSIL
                                                                                                                                                                                                                                                                                                                                                                   HIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQQQBGYRGTVNTIMNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESFWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECQRWDLQHPHQHPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVRTCIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNPDGDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD
                                                                                                                                                                                                                                                                                                                                                                                                                                    FTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRGKGEGYRGTANTTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDGSEAPWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPGKFLDQGLDDNYCRNPDGSERPWCYTTDPQIEREFCDLPRCGSEAQPRQEA--TTVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VADAEECAGRC----GPLMDCRAFHYNVSSHGCQLLPWTQHSPHTRLRRSGRCDLFQKKD
                                                                                                                                                                                                                                                                                                                                                                                                      FTLRPGMRAAFCYOIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQCQRWSAETPHKPQ
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 homologue
                                                                                                             Xenopus.
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E -> K (in_dbsNp:7798).

/FTId=VAR_014569.

R -> G (in_Ref. 3).

C -> E (in_Ref. 3).

R -> E (in_Ref. 3).

PS -> SL (in_Ref. 3).

PS -> SL (in_Ref. 3).

W -> E (in_Ref. 3).
                                                                                                                                                                                             Last sequence update)
Last annotation update)
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By similarity.
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By similarity.
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Note: Note
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N-linked
Y -> C.
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Pred. No. 3.8e-80;
0; Mismatches 148
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                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          596ED21F180290E4
                                 DOI=10.1016/0925-4773 (95) 00458-0;
 growth
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                                                                                                                                Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148;
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                                                                                                                                                                                                                                                                                                                                            457
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WI specifically expressed in the presumptive neural plate during with the presumptive neural plate during the Mech. Dev. 54:23-37(1996).

MEMBLY Y08734; CAA69989.1; -.

MEROPS; S01.977; -.

MEROPS; S01.0975; F:calcium ion binding; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

MEGO; GO:0008233; F:septidase activity; IEA.

MEGO; GO:000309; F:thrombin activity; IEA.

MEGO; GO:0004295; F:thrombin activity; IEA.

MEGO; GO:0004295; F:thrypsin activity; IEA.

MEGO; GO:0007596; P:blood coagulation; IEA.

MECOPORTO; IPRO00301; MATINGLE.

MINTERPO; IPRO03014; PAN.

MINTERPO; IPRO03014; PAN.

MINTERPO; IPRO03609; PAN app.

MINTERPO; IPRO03609; PAN app.

MEROPORTO; IPRO03609; PAN app.

METOPORTO; IPRO03609; PEPTIdase_S1A.

MINTERPO; IPRO03609; PEPTIDASE_S1A.

MECOPORTO; IPRO0369; PEPTIDASE_S1A.

MECOPORTO; IPRO0369; PEPTIDASE_S1A.

MECOPORTO; IPRO0369; PEPTIDASE_S1A.

MECOPORTO; IPRO0369; PEPTIDASE_S1A.

MEROPORTO; IPRO03669; PEPTIDASE_S1A.

MEROPORTO; IPRO03669; PEPTIDASE_S1A.

MEROPORTO; IPRO03669; 
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Best Local Similarity
Matches 199; Conserv
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SMART; SM000473; PAN AP; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE 1; 4.

PROSITE; PS50070; KRINGLE 2; 4.

PROSITE; PS50948; PAN; 1.

PROSITE; PS50948; PAN; 1.

PROSITE; PS50948; PAN; 1.

PROSITE; PS50948; PS50948
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                                                 324
                                                                                                                                                                                                                                                                                                             302
                                                                                                                                                                                                                                                                                                                                                                                                               267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 TRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEH
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ELYRGRVSKTRKGIMCRRWEEKQNDLELSLA-QPYLVPLEENYCRNPDRDSHGPWCYTMD
                                                                                                                                                                                               RFLPEKYPCKGLDENYCRNPVGSEAPWCFTTLKNMRMAYCFQIKRCTDDVVEPECYHGNG
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Aar40862 Competati	Aar20005 Human hep	Aar25676 Recombina	Aau04275 Nuclear l	œ	0	Aay98485 Hepatocyt	Adm83266 Human NK4	Ade37393 Human hep	Aar32710 Haematopo	Aaw59923 Human leu	Aar21142 Human TCF	Aay57174 N-termina	Add69672 Chimeric	Aay06622 HGF-MSP h	Aay06621 HGF-MSP h	Aaw76690 Human pla	Aar82685 Tumour cy	Aar57026 Human wil	Aar57028 Human mod	Aar57027 Human mod	Aar25677 Recombina	Aar15624 Human leu	Aar07144 Tumour cy	Adm83267 Human NK4	ription

The present invention provides a therapeutic agent NK4 polypeptides and their encoding polynucleotides. The invention is useful for producing a medicament for preventing or treating diseases caused by neovascularisation such as ovarian cancer, pancreatic cancer, stomach cancer, gallbladder cancer, renal cancer, prostatic cancer, breast cancer, gallbladder cancer, hepatic cancer, oral cavity cancer, colon cancer, colorectal cancer, hepatic cancer, oral cavity cancer. The invention i also useful in gene therapy. The present sequence is human NK4 protein.

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Disclosure; Page 17-19; 27pp; English.

treating New NK14

gene, useful for producing a medicament for preventing diseases caused by neovascularization, e.g. cancer.

or

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Aar15623	Aar10656	Aay57173	Ads19044	Adt89322	Adm97652	Adb61534	Abp58128	Aaw39207	Aaw42998	Aaw58696	Aaw59922	Aaw00338	Aaw00340	Aar87523	Aar87525	Aar87524	Aar87522	Aar42062	
Human leu	Hepatic p	N-termina	Chimeric				Human hep	Human hep	Recombina	Human hep	Human leu		Wild type		Mutant he	Mutant h	Mutant he	Vascular	

## ALIGNMENTS

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RESULT 1
ADM83267
ID ADM8
NK4 gene; neovascularisation; ovarian cancer; pancreatic cancer; stomach cancer; gallbladder cancer; renal cancer; prostatic cancer; breast cancer; sophageal cancer; hepatic cancer; oral cavity cancer; colon cancer; colorectal cancer; sarcoma; glioma; melanoma; gene therapy;
                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004 (first entry)
                                                                                                                               N-PSDB; ADM83265.
                                                                                                                                      WPI; 2003-897946/82
                                                                                                                                                       Nakamura T, Matsumoto
                                                                                                                                                                                                                                      28-AUG-2003.
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                           WPI; 1990-304990/40.
P-PSDB; AAR07144.
                                                                                              Higashio K,
                                                                                                                                                                                          10-MAR-1989;
16-JAN-1990;
                                                                                                                                                                                                                                                                   10-MAR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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31-JAN-1991
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                                                                                                                                                 25-MAR-2003
18-MAR-1992
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Pred. No. 1.4e-163;
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Human leukocyte-derived HGF

growth

factor;

liver; hepatoma

encoded by clone

EP461560-A Homo sapiens Hepatocyte

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RESULT 4
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Best Local S
Matches 441
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Sakaguchi M,
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Asami O;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant human hepatocyte growth factor and DNA encoding it - useful for diagnosis and treatment of hepatic disease and transgenic animal
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(NAKA/) NAKAMURA T.
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              KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN
                                                             HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQI PNCDMSHGQDCYRGNG
                                                                                                               HTRWEYCAIKTCADNIMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE
                                                                                                                                                                  ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
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reagent; drug.
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Pred. No. 1.4e-163;
1; Mismatches 0;
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oligosaccharide chain - have
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Takahira R,
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Ueda M,
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we longer biological
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Pred. No. 1.4e-163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified tumour cytotoxic factors with loss of oligosaccharide chain - have longer biological
                                                                                                                                                                                                                                                                                                   Sequence
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Takahira R,
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                                                                                                                                      ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
                                                        WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG
                                                                                                                   ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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Pred. No. 1.4e-163;
1; Mismatches 0;
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Higashio
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                                                                                                                                                                             Query Match
Best Local Similarity
Matches 441; Conser
                                                                                                                                                                                                                                                                                                                              This TCF sequence may be modified in that the AA residues responsible for binding of N-linked oligosaccharide chains are modified so that at least one of the N-linked oligosaccharide chains is prevented from binding to TCF. Ser-563 may be substituted with Ala (AAR57027) or Asn-289 substituted with Gln (AAR57028). (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified tumour cytotoxic oligosaccharide chain - ha
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19-MAR-1995
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                                                                                                             ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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                     ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                      QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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                                                                                                                                                                               Conservative
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Oogaki
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we longer biological
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                                                                                                                                                                             Score 2576; DI
Pred. No. 1.4e
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RESULT 8
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XX TUMO
XX TUMO
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XX MONC
XX HOMC
XX HO
                                                                                         This sequence represents human tumour cytotoxic factor-II (TCF-II). TCF-II II has potent antitumour activity and growth stimulation activity. TCF-II is a member of the hepatocyte growth factor family (HGF). This sequence is used as an antigen to produce TCF-II specific antibodies that show no affinity to human HGF. The monoclonal antibody (MAb) was produced using hybridoma techniques. The MAbs were screened using solid phase EIISA with an increased selectivity. The MAb can be used for the selective determination or purification of TCF-II without any influence from the presence of HGF. The TCF-II can be used as an antitumour agent, a wound be the control of the selective to the selective can be used as an antitumour agent, a wound be the control of the selective to the selective can be used as an antitumour agent, a wound be the control of the selective can be used as an antitumour agent, a wound be a selective can be used as an antitumour agent, a wound be a selective can be used as an antitumour agent, a wound be a selective can be used as an antitumour agent.
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   Sequence
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RESULT 9
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ID AAW76690
ID AAW76690
AC AAW7
XX AAW7
DT 25-M
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XX Huma
XX Homc
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Best Local Similarity
Matches 441; Conserv
                     N-PSDB; AAV61952
                                         WPI; 1998-567711/48
                                                                                                                                                                                          05-MAY-1994;
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29-JAN-1999
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                                                                           Rubin JS,
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                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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variant; wound
                                                                             Chan
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                                                                                                                                                                                                                                                                                                                                                                                                                      PLGF; endothelial cell;
healing.
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AAYO6621
ID AAYO6
XX AAYO6
XX 26-OC
XX 26-OC
XX Alpha
KW macrc
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OS Synth
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Homo sapiens. Synthetic.

Peptide Domain

/note= 1. .3.1

"HGF

alpha chain"

"HSP alpha signal peptide"

Location/Qualifiers

therapy

Alphabet-1; human; hepatocyte growth factor; HGF; MSP; macrophage stimulating protein; apoptosis; chemotherapy;

toxicity;

26-OCT-1999

(first

entry)

HGF-MSP hybrid

protein alphabet-1 factor.

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FFXSXSSSSSSSXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Human plasminogen-like growth factor PLGF is used in the st of the growth of endothelial cells or epithelial cells other th hepatocytes. This involves contacting the cells with the PLGF pits allelic or splice variants. The growth factor is useful for stimulating wound healing in endothelial or epithelial tissue. on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulation of endothelial or epithelial cell growth - like growth factor protein.
 AAY06621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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 standard;
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                                                                                                             PLIPWDYCPISRCEGDTTPTIV
                                                                                                                                               KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN
                                                                                                                                                                 KNYMGNISQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN
                                                                                                                                                                                                                                                                               HTRWEYCAIKTCADNTWNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE
                                                                                                                                                                                                                                                                                                                                             ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
                                                                                                                                                                                                                                                                                                                                                                                                            WSSMI PHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDI PQCSEVECMTCNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       723 AA;
                                                                                  PLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                                                                                 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG
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protein;
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Pred. No. 1.4e
1; Mismatches
     729
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     B
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1.4e-163;
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Query Match
Best Local Simi
Matches 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins are used for the prevention or treatment of chemotherapeutic-induced toxicity such as myelotoxicity, hepatotoxicity, nephrotoxicity, mucotoxicity and neurotoxicity (claimed). They protect cells from death (apoptosis) induced by chemotherapy of, e.g. tumors. In particular, they can be used for expansion of marrow precursors, to increase proliferation of the haematopoietic precursors or to stimulate their entry in the cycle. By modification of the proteolytic site, hybrid factors can be obtained which are activated by proteases of the endoplasmic reticulum (such as furines) during their synthesis. When the proteolytic site is removed, permanently immature forms of the factors can be obtained, having a potential partial agonistic or antagonistic activity. Different functional domains can be combined so as to modulate the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 729 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and thereby induce biological responses which are synergistic and selective compared with the natural factor and truncated forms of the proteins. The portions of DNA encoding the various portions of alphabet-1 are obtained by PCR amplification of HGF or MSP cDNA and recombined to obtain a hybrid DNA (see AAX87676). Expression vectors, prokaryotic or eukaryotic host cells and a process for preparing recombinant proteins from HGF and MSP are claimed. Alphabet-1 and other HGF-MSP recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of alphabet-1 factor, a recombinant protein composed of the hepatocyte growth factor (HGP) alpha chain (i.e. protein composed of the hepatocyte growth factor (HGP) alpha chain (i.e. the signal sequence, hairpin loop grotein (MSP) beta chain and a site of HGF, the macrophage stimulating protein (MSP) beta chain and a polyhistidine tag sequence. This structure allows the recombinant protein to interact with both the HGF receptor (Met) and the MSP receptor (Ron)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 54-56; 63pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX87676
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                                   WSSMI PHEHSYRGKDLOENYCRNPRGEEGGPWCFTSNPEVRYEVCDI PQCSEVECMTCNG
                                                                                                                          ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                                                                                                   QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                       ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
Michieli
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492. .7
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/note= "MSP beta chain"
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                                                                                                                                                                                                                                                                                                          Score 2576; DE Pred. No. 1.4e-1; Mismatches
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Recombinant proteins from recombination of HGF and MSP structural domains, useful for protecting cells against apoptosis induced by
                                  N-PSDB; AAX87677
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Synthetic.
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                                              WPI; 1999-494091/41
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                                                                                                                                                                                                                   Peptide
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                                                                    Michieli
                                                                                                                                                                                                                                                                                                                                                                                                                                   stimulating protein; apoptosis; chemotherapy; toxicity;
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                                                                                                               98IT-MI000180
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                                                                                                                                                                                                       /note= "polyhistidine tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 441;
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Pred. No. 1.4e-163;
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 441; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel drug comprising a protein forming hollow nanoparticles and capable of recognising specific cells which is fused with therapeutic substances for transfer into cells. The protein is particularly hepatitis B virus (HBV) surface antigen protein (HBsAg). The drugs of the invention demonstrate hepatotropic activity and may be useful for disease treatment, particularly in the therapy of liver diseases. The protein of the invention and subsequently the drug, has selectivity and specificity in targeting cells or tissues for delivering drugs fused with the specific nanoparticle-forming proteins, therefore, gene therapy can be achieved without needing surgery and with reduced side-effects. The current sequence is that of the chimeric HGF/HBsAg L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drugs comprising protein to form hollow nanoparticles with therapeutic substances encapsulated capable of recognizing target cells or tissues specifically and selectively, applicable in disease treatment.
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1109
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Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                 protein (SEQ ID 20) of the invention.
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liver disease; gene t
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                                                       ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
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Pred. No. 2.2e-163;
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HGF.
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                        macular degeneration and excess scarring during wound healing), as a contraceptive, to modulate abnormal proliferation or vascularization (e.g. psoriasis, Osler-Webber syndrome, myocardiac angiopoiesis, peripheral angiectasis, haemophiliac rheumatism, angiopoiesis of the eye, angiofibroma, benign tumor and wound granulation), or to treat or prevent conditions due to the over-stimulation of endothelial cells (e.g. Crohn's disease adenomatous sclerosis, gastrointestinal healing, toughening of
                                                                                                                                                                                                                                   The invention relates to neovascularization inhibitors comprising a polypeptide (A) with the amino acid sequence of N-terminal region of hepatocyte growth factor (HGF), or a polypeptide with an amino acid sequence derived from (A) which has antagonistic activity against HGF via the cMet-HGF receptor. The polypeptides can be used as neovascularization inhibitory factors (e.g. for preventing and treating rhemmatoid arthritis, diabetic conjunctivitis, neonatal conjunctivitis, senile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neowascularization; inhibitor; hepatocyte growth factor; HGF; CMet-HGF receptor; rheumatoid arthritis; diabetic conjunctivitis; neonatal conjunctivitis; senile macular degeneration; scarring; mwound healing; contraceptive; vascularization; Crohn's disease; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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present sequence represents
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                       Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TCF-II.
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20-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR21142 standard;
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                                                                                                                                                             13-JUL-1990;
                                                                                                                                                                                                       23-JAN-1992
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                       Oogaki F,
                                                                                                                                                                                                                                                                                                                                                                                                                                growth
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                         Takaoka
                                                                                                                                                                                                                                                                                              sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A human foetal lung fibroblast library was screened with a synthetic probe coding for the N-terminal sequence of TCF-II. A cDNA clone was isolated and sequenced. The coding sequence can be incorporated into a plasmid and transformed into a microorganism for production of TCF-II. The protein itself can be used as a liver cell growth factor or a tumous cell killing factor. See also AAQ21067-9. (Updated on 25-MAR-2003 to
                                                                                                                                                      25-MAR-2003
21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6;
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                                   Homo sapiens
                                                                                     Hepatocyte-derived
                                                                                                                     Human leukocyte-derived hepatocyte growth factor HCL2
                                                                                                                                                                                                         AAW59923;
                                                                                                                                                                                                                                         AAW59923 standard;
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DB; AAQ21066.
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Sakaguchi M,
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## ALIGNMENTS

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LENGTH: 489
TYPE: PRT
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                                                                                                                              Query Match 99.8
Best Local Similarity 99.8
Matches 441; Conservative
                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAKAMURA Toshikazu
APPLICANT: MATSUMOTO Kunio
APPLICANT: PUKUTA Kazuhiro
APPLICANT: PUKUTA Kazuhiro
TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain
FILE REFERENCE: 2004-1328A/MMC/01736
CURRENT APPLICATION NUMBER: US/10/926,088A
CURRENT FILING DATE: 2004-08-26
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens FEATURE:
                                                                                                                                                                                                                 OTHER INFORMATION: alpha-chain of human hepatocyte OTHER INFORMATION: type
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ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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Pred. No. 9.6e
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                                                                                                                                DB 18;
9.6e-210;
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FILE REFERENCE: 2520-0101P
CURRENT APPLICATION NUMBER: US/08/605,221
CURRENT FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 4
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: HGF-B (five amino acids
US-08-605-221-4
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US-08-605-221-4
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Publication No. US20030060403A1
GENERAL INFORMATION:
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TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
FILE REFERENCE: 2520-0101P
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                HTRWEYCAIKTCADNTWNDTDVPLETTECIQGQEGYRGTVNTIWNGIPCQRWDSQYPHE
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  KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN
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Pred. No. 1.5e-209;
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FILE REFERENCE: P023P01/US
CURRENT APPLICATION NUMBER: US/10/509,247A
CURRENT FILING DATE: 2004-09-28
PRIOR APPLICATION NUMBER: PCT/JP03/02602
PRIOR FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: PCT/JP03/02602
PRIOR FILING DATE: 2003-03-29
PRIOR FILING DATE: 2003-03-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3:3
SEQ ID NO 20
LENGTH: 1109
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US-10-509-247A-20
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Best Local Similarity 99.8%;
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APPLICANT: Ueda, Masakazu
APPLICANT: Seno, Masakazu
APPLICANT: Seno, Masakazu
APPLICANT: Tada, Hiroko
APPLICANT: Tada, Hiroko
TITLE OF INVENTION: DRUG CONTAINING HOLLOW PROTEIN NANOPARTICLES OF PARTICLE-FORMING
TITLE OF INVENTION: PROTEIN, FUSED WITH DISEASE-TREATING TARGET-CELL-SUBSTANCE
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ORGANISM: Artificial Sequence
FEATURE:
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PLIPWDYCPISRCEGDTTPTIV
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Kondo, Akihiko
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Pred. No. 2.6e-209;
1; Mismatches 0;
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RESULT 5
US-10-081-309-2
; Sequence 2, Application US/10081309
; Publication No. US20030012775A1
; GENERAL INFORMATION:
APPLICANT: Hoffmann-La Roche Inc.
TITLE OF INVENTION: PEG Conjugates of NK4
; FILE REFERENCE: 20859
; CURRENT APPLICATION NUMBER: US/10/081,309
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CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: UP 300728
PRIOR FILING DATE: 1995-10-24
PRIOR PELING DATE: 1995-10-24
PRIOR FILING DATE: 1996-10-3105
PRIOR PILING DATE: 1996-10-32
PRIOR APPLICATION NUMBER: US 09/471,032
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
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; TYPE: PRT
; ORGANISM: Homo s
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APPLICANT: NAKAMURA, Toshikazu
TITLE OF INVENTION: Anti-Cancer Agent
FILE REFERENCE: 4373-0101P
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Best Local Similarity
Matches 441; Conserv
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Sequence 1, Application US/10926088A

Publication No. US20050164918A1

GENERAL INFORMATION:
APPLICANT: MACKAUMA Toshikazu
APPLICANT: MACKAUMA Toshikazu
APPLICANT: FUKUTA Kazuhiro

TITLE OF INVENTION: A Begment of glycosylation-deficient HGF alpha-chain
FILE REFERENCE: 2004-1328A/WMC/01736

CURRENT APPLICATION NUMBER: US/10/926,088A

CURRENT APPLICATION NUMBER: US/10/926,088A

CURRENT FILING DATE: 2004-08-26

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 1

LENGTH: 494

TYPE: PRT

ORGANISM: Homo Sapiens
FEATURE:
FEATURE:
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                                                                  ; OTHER INFORMATION: alpha-chain of human hepatocyte growth factor US-10-926-088A-1
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 Query Match
Best Local S
Matches 441
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn verseq ID NO 2
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 Score 2563.5; DB 10
Pred. No. 1.1e-208;
1; Mismatches 0;
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Pred. No. 9.96
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APPLICANT: Ulrich Kettling
APPLICANT: Ulrich Kettling
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND
FILE REFERENCE: 04156,0002U4
CURRENT APPLICATION NUMBER: US/10/872,198
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/543,518
PRIOR FILLING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR FILLING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILLING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR FILLING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILLING DATE: 2003-16-18
PRIOR FILLING DATE: 2003-16-18
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US-10-872-198-120
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; ORGANISM: Homo
US-10-872-198-120
                                                                      Query Match
Best Local S
Matches 441
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                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 120
LENGTH: 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ulrich HAUPTS
APPLICANT: Andre KOLTERMANN
APPLICANT: Andreas SCHEIDIG
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o. US20050002897A1
                                                                          Conservative
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98.7%;
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                                                                      Score 2563.5; DB 1
Pred. No. 1.8e-208;
1; Mismatches 0;
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SEQ ID NO 120
SEQ ID NO 120
LENGTH: 726
TYPE: PRT
ORGANISM: Homo sapiens
US-11-021-951-120
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                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/021,951
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: 10/872,198
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-02-11
PRIOR PPLICATION NUMBER: 60/543,518
PRIOR PPLICATION NUMBER: 60/524,960
PRIOR PPLICATION NUMBER: 60/524,960
PRIOR FILING DATE: 2003-11-25
PRIOR PPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR PRIOR DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR PILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-06-18
NUMBER: OF SEQ ID NOS: 191
PRIOR PRIOR PRIOR DATE: 2003-06-18
NUMBER: OF SEQ ID NOS: 191
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US-11-021-951-120
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                Query Match
Best Local (
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 Matches
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APPLICANT: KOLTER
APPLICANT: SCHEID
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APPLICANT: SCHEIDIG, Andreas
APPLICANT: VOTSMEIER, Crinistian
APPLICANT: Ketthing, Ulrich
APPLICANT: COCO, Wayne Michael
TITLE OF INVENTION: New Biological Entities And
TITLE OF INVENTION: And Diagnostic Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 04156.0002U5
Local Sim hes 441;
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o. US20050175581A1
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                99.4%;
98.7%;
<u>1</u>
Score 2563.5; DB 20
Pred. No. 1.8e-208;
1; Mismatches 0;
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                                   DB 20;
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   Indels
                                   Length
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APPLICANT: (NAKAMURA, TOShikazu
FITLE OF INVENTION: THERAPEUTIC AGENT FOR DIS
FILE REFERENCE: 2520-0101P
CURRENT APPLICATION NUMBER: US/08/605,221
CURRENT FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 728
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: HGF-A (Full length HGF)
US-08-605-221-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-605-221-2
US-08-605-221-2
; Sequence 2, Application US/08605221
; Publication No. US20030060403A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 441; Conserv
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                                                                   MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC
                                                                                                       WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
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APPLICANT: Hambor, John E.

APPLICANT: FPIZER INC.

APPLICANT: Roach, Marsha L.

APPLICANT: Roach, Marsha L.

TITLE OF INVENTION: GROWTH AND DIFFERENTIATION OF FILE REFERENCE: PC25028A

CURRENT APPLICATION NUMBER: US/10/813,805

CURRENT APPLICATION NUMBER: US 60/459,449

PRIOR APPLICATION NUMBER: US 60/459,449

PRIOR FILING DATE: 2003-03-31

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin version 3.2

SEQ ID NO 10

LENGTH: 728

TYPE: PRT

ORGANISM: Homo sapiens

US-10-813-805-10
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US-10-813-805-10
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Best Local Sim
Matches 441;
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Publication No. US20040191902A1
GENERAL INFORMATION:
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                                                                                                                                             QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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                   CYTGNPLIPWDYCPISRCEGDTTPTIV 442
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                                                                YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
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Pred. No. 1.8e-208;
1; Mismatches 0; I
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APPLICANT: Gherardi, Ermanno
APPLICANT: Lietha, Daniel
APPLICANT: Blundell, Thomas L
APPLICANT: Chirgadze, Dinitry Y
ITILE OF INVENTION: The NK1 Fragment of Hepatocyte Growth Factor/Scatter
ITILE OF INVENTION: Factor (HgF/SF) and Variants Thereof, and Their Use
FILE REFERENCE: 2502489 991180
CURRENT APPLICATION NUMBER: US/10/475,616
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: PCT/GB02/01941
PRIOR APPLICATION NUMBER: GB 0110430.6
PRIOR APPLICATION NUMBER: GB 0110430.6
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
LENGTH: 728
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                                         ; Sequence 7, Application US/10498332
; Publication No. US20050113284A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Motonao
; APPLICANT: Higuchi, Toshio
; APPLICANT: Yoshio
; APPLICANT: Yoshio
; APPLICANT: Yoshio
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US-10-498-332-7
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; ORGANISM: Homo
US-10-475-616-2
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Publication No. US20040236073A1
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INV
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Best Local Similarity
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OF INVENTION:
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                Higuchi, Toshio
Yamasaki, Yoshiki
Orita, Takuya
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 PHARMACEUTICAL AGENTS AND METHODS
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Pred. No. 1.8e-208;
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CURRENT FILING DATE: 2004-06-11
PRIOR APPLICATION NUMBER: PCT/JP02/13014
PRIOR FILING DATE: 2002-12-12
PRIOR APPLICATION NUMBER: JP 2002-352924
PRIOR FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
PRIOR PPLICATION NUMBER: JP 2001-380158
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 728
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; TYPE: PRT
; ORGANISM: Homo s
US-10-498-332-7
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US-10-133-912-18
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Best Local Similarity 98.7%;
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                                                           Ueda, Masatsugu
Higashio, Kanji
Yamashita, Yasushi
TITLE OF INVENTION: TCF MUTANT
NUMBER OF SEQUENCES: 25
                CORRESPONDENCE ADDRESS:
ADDRESSEE: Burgess, Ry
STREET: 370 Lexington
                                                                                                                                                                                            APPLICANT:
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 CITY: NEW
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                                                                                                                                                           Yamaguchi, Kyoji
Goto, Masaaki
                                                                                                                                          Murakami, Akihiko
 YORK
                Ryan and Wayne
on Avenue, Suit
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                   Suite
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E OF INVENTION: TISSUE AND VASCULAR REGENERATION REFERENCE: 14539-016US1
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YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
                                                                                                 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC
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Pred. No. 1.8e-208;
1; Mismatches 0;
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RESULT 14
US-10-133-912-19
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Sequence 19, Application US/10133912 Publication No. US20020165358A1 GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/700,519
FILING DATE: 26-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milton J.
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-5240PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-683-8150
TELEPHONE: 212-532-4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/5 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: WORD FOR WINDOWS
SOFTWARE: MICROSOFT WINDOWS 98
CURRENT APPLICATION DATA:
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FILING DATE: 25-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                       397
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Pred. No. 1.1e-207;
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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-133-912-19
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FILING DATE: 26-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milton J.
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-5240PC
REFERENCE/DOCKET NUMBER: U-Wp-5240PC
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-633-64150
TELEFAX: 212-632-4485
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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TITLE OF INVENTION: TCF MUTANT
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                         HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE
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                                                               HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG
                                                                                                                  HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE
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STREET: 370 Lexington Avenue, Suite
CITY: NEW YORK
STATE: NEW YORK
KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN
                                                                                                                                                                                              ESYRGLMDHTESGK1CQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
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TYPE: AMINO ACID
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COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: WORD FOR WINDOWS
SOFTWARE: MICROSOFT WINDOWS 98
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Higashio, Kanji
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Pred. No. 1.7e-207;
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US-10-149-103A-1
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APPLICANT: Sim, Kim Lee
APPLICANT: Sim, Kim Lee
APPLICANT: Day, Clara
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
FILE REFERENCE: 05213-0592 43170-274540
CURRENT APPLICATION NUMBER: US/10/149,103A
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/US00/34039
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 727
TYPE: PRT
CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10149103A Publication No. US20040121945A1
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Matches 433;
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Best Local Similarity 97.1%;
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                                                                                                                                                                                                                                                                                                                            TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 236
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                                                                              YTGNPLIPWDYCPISRCEGDTTPTIV 442
                                                                                                                       RGNGKNYMGNLSQTRSGLTCSMWNKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWC
                                                                                                                                                                                                     YPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCY
                                                                                                                                                                                                                                               TLDPHTRWEYCAIKTCADNTVNDTDVPMETTECIQGQGEGYRGTANTIWNGIPCQRWDSQ 332
                                                                                                                                                                                                                                                               TLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQ 296
                                                                                                                                                                                                                                                                                                          TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY
                                                              YTGNPLIPWDYCPISRCEGDTTPTIV
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               2005, 07:42:28
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Pred. No. 2e-205;
Pred. No. 2e-205; Indels
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Title:
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Maximum Match 100%
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/FUTUS_COMB.pep:*
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    2005, 05:58:32; Search time 1360.31 Seconds
(without alignments)
    24.255 Million cell updates/s

 GenCore version (c) 1993 - 2005
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US-08-404-643-1
US-09-601-040A-10
US-09-601-040A-10
US-09-601-040A-2
US-09-601-040A-2
US-09-601-040A-3
US-08-209-337B-3
US-08-209-337B-3
US-08-209-337B-3
US-08-460-890A-50
US-08-167-641C-50
US-08-167-783A-2
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Sequence 6, Appli
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Sequence 11, Appli
Sequence 2, Appli
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Sequence 3, Appli
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Sequence 2, Appli
Sequence 3, Appli
Sequence 11, Appl
Sequence 12, Appli
Sequence 13, Appl
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sequence
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D Qy	Db Qy	Qу	Db Qy	Qy db	Qy Db	Qy Db	Query Best Match	RESULT US-09-6 ; Seque ; Seque ; Paten ; GENER ; APPL ; TITL ; FITL ; CURR		2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRN	301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPN 	241 HTRWEYCAIKTCADNTWNDTDVPLETTECIQGQGEGYRGTVNTIWNG	181 ESYRGIMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRN 	121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCD	61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVS:	1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGI 	ery Match 99.9%; Score 2576; DB 4; Lengt st Local Similarity 99.8%; Pred. No. 1.1e-213; tches 441; Conservative 1; Mismatches 0; Inde	ULT 1 09-601-040A-27 equence 27, Application US/09601040A atent No. 6730657 atent No. 6730657 ENERAL INFORMATION: APPLICANT: MEDICO, Enzo et al. APPLICANT: MEDICO, Enzo et al. FILE REFERENCE: 0471-0161P CURRENT APPLICATION NUMBER: US/09/601,040A CURRENT FILING DATE: 2000-09-08 MUMBER OF SEQ ID NOS: 28 SOFTWARE: PatentIn version 3.0 EQ ID NO 27 TYPE: PRT ORGANISM: Homo sapiens 09-601-040A-27	ALIGNMENTS	28 1460 56.6 563 4 US-09-600-991-4 29 1433.5 55.6 290 4 US-08-484-841A-8 30 1171 45.4 711 1 US-08-184-012C-8 31 1171 45.4 711 1 US-08-334-177-2 32 1171 45.4 711 2 US-08-66-082B-1 33 1171 45.4 711 2 US-08-766-982-2 34 1171 45.4 711 2 US-08-766-982-2 35 1171 45.4 711 3 US-09-296-219-2 36 1171 45.4 711 4 US-09-601-040A-12 37 1171 45.4 711 4 US-09-949-016-6981 38 1171 45.4 711 4 US-09-949-016-6981 39 1114.5 43.2 716 2 US-08-766-982-1 40 1114.5 43.2 716 2 US-08-766-982-1 41 1054.5 40.9 790 4 US-08-991-7219-1 42 1039.5 40.3 812 1 US-08-248-629A-1 43 1039.5 40.3 812 1 US-08-452-260-1 45 1039.5 40.3 812 1 US-08-326-785-1
NPDDDAHGPWCYTGN 420               NPDDDAHGPWCYTGN 451	NCDMSHGQDCYRGNG 360                NCDMSHGQDCYRGNG 391	NGIPCQRWDSQYPHE 300                  NGIPCQRWDSQYPHE 331	RNPDGQPRPWCYTLDP 240	DIPOCSEVECMTCNG 180	KGTVSITKSGIKCQP 120           KGTVSITKSGIKCQP 151	NKGLPFTCKAFVFDK 60 	h 487; ls   0; Gaps   0;	Đ		Sequence 4, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 20, Appli Sequence 20, Appli Sequence 12, Appli Sequence 12, Appli Sequence 1, Appli

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GENERAL INFORMATION:
APPLICANT: MEDICO, Enzo et al.
TITLE OF INVENTION: Recombinant Proteins from HG
FILE REFERENCE: 0471-0161P
CURRENT FILING DATE: 2000-09-08
UNMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 717
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-601-040A-8
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Sequence 8, Application US/09601040A
Patent No. 6730657
GENERAL INFORMATION:
APPLICANT: MEDICO, Enzo et al.
TITLE OF INVENTION: Recombinant Proteins from
FILE REFERENCE: 0471-0161P
CURRENT APPLICATION NUMBER: US/09/601,040A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 28
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Best Local S
Matches 441
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OTHER INFORMATION: Recombinant sequence derived
-09-601-040A-6
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o. 6730657
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Pred. No. 1.8e-213;
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; TYPE: PRT
; ORGANISM: Artificial S
; FEATURE:
; OTHER INFORMATION: Rec
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                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: HIGASHIO, KANJI
APPLICANT: NAGAO, MASAYA
APPLICANT: NAGAO, MASAYA
APPLICANT: TAKAOKA, HIROAKI
APPLICANT: TSUDA, EISUKE
TITLE OF INVENTION: PLASMIDS,
TITLE OF INVENTION: PLASMIDS,
TITLE OF INVENTION: SUBSTANCE
NITMED OF STRUENCES
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 1 Patent No.
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Best Local :
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COUNTRY: USA
ZIP: 22201
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHIT
STREET: 2200 CLARENDON
                                                                                                    CITY: ARLINGTON STATE: VA
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Best Local S
Matches 441
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OTHER INFORMATION: /
OTHER INFORMATION: SI
FEATURE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00942
FILING DATE: 15-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185852-1990
FILING DATE: 13-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 64191
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
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REGISTRATION NUMBER: 17,746
REFERENCE/DOCKET NUMBER: WAK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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LOCATION: 605..623
OTHER INFORMATION: OTHER INFORMATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Domain LOCATION: 393..405 OTHER INFORMATION:
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Similarity 99.8%;
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                   HDMTPENFKCKOLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG
                                                                                    HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE
                                                                                                                                 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
                                                                                                                                                    ESYRGLMDHTESGKI CQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
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 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG
                                                                 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE
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Fibroblast
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SEQUENCE IN ALPHA-CHAIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2576; DB 1; Length 723; Pred. No. 1.9e-213;
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US-08-290-937B-1
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Patent No. 5648233
GENERAL INFORMATION:
                                                                                                                                                                       Matches 441;
                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,9371
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 248-71
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 02110
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121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG
                                                                            61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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                                                ARKOCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCOP
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UEDA, MASATSUGU
HIGASHIO, KANJI
NVENTION: MODIFIED T
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125 High St.
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MASUNAGA, HIROAKI
TAKAHIRA, REIKO
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                                                                                                                                                                                                                                                                 SS: single
linear
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, NOBUYUKI
                                                                                                                                                                                    99.9%;
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                                                                                                                                                                      Score 2576; DB 1;
Pred. No. 1.9e-213;
1; Mismatches 0;
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,937B
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ 1D NO: 2:
OFFICE OF THE PARTY OF 
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    Query Match
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APPLICANT: TAKAHIRA, REIKO
APPLICANT: OCCAKI, FUMIKO
APPLICANT: UEDA, MASATSUGU
APPLICANT: HIGASHIO, KANJI
TITLE OF INVENTION: MODIFIED TO
NUMBER OF SEQUENCES: 13
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                                                                                                                        LENGTH: 723 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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CITY: Boston
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RESULT 7
US-08-404-643-1
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APPLICANT: HIGASHIO, KANJI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: OCGAKI, FUMIKO
TITLE OF INVENTION: MONOCLON
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1,
Patent No.
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Matches 441; Conservative
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION NUMBER: US/08/404,643
FILLING DAYTE: 15-MAR-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-034 (33)
TELEFAX: (617)-248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (617)-248-7000
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                                                                                                                                                                                                                                                                                                                                                                             STREET: 53 ST.
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
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                   (617)-248-7100
(7) TD NO: 1:
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1; Mismatches 0;
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APPLICANT: Kinosaki, Masahiko
APPLICANT: Kinosaki, Hiromi
APPLICANT: Masanuga, Hiromi
APPLICANT: Masanuga, Hiroaki
APPLICANT: Mobayashi, Funie
APPLICANT: Yamaguchi, Kyoji
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Agent for Preventing and/or Treating Renal Disease
FILE REFERENCE: FJN-069
CURRENT APPLICATION NUMBER: US/09/194,326
CURRENT APPLICATION NUMBER: PCT/JP98/01221
EARLIER APPLICATION NUMBER: PCT/JP98/01221
EARLIER FILING DATE: 1998-03-20
EARLIER FILING DATE: 1998-03-20
EARLIER FILING DATE: 1997-03-28
NUMBER: OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
FFATURF:
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; STRANUEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-404-643-1
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US-09-194-326-1
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; OTHER INFORMATION:
US-09-194-326-1
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Best Local Similarity 99.8
Matches 441; Conservative
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Pred. No. 1.9e-213;
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2576;
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APPLICANT: MEDICO, Enzo
APPLICANT: MICHIELI, Paolo
APPLICANT: COLLESI, Chiara
APPLICANT: COLLESI, Chiara
APPLICANT: CASELIJ, Gianfranco
APPLICANT: CASCLIJ, Gianfranco
TITLE OF INVENTION: RECOMBINANT PROTEINS DERIVED FRO
FILE REFERENCE: 0471-0162p
CURRENT APPLICATION NUMBER: US/09/600,991
CURRENT APPLICATION NUMBER: 2001-08-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
US-09-600-991-18
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US-09-600-991-18
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Best Local Similarity
Matches 441; Conserv
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WSSMI PHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDI PQCSEVECMTCNG
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ilarity 99.8%;
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                                                                                                                                                                                     Score 2576; DB 4;
Pred. No. 1.9e-213;
1; Mismatches 0;
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1; Mismatches 0;
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Sequence 4, Application US/08605221

Patent No. 6699837

GENERAL INFORMATION:
APPLICANT: NAKAMURA, Toshikazu
TITLE OF INVENTION: THERAPBUTIC AGENT FOR DISORDER IN BRAIN
FILE REFERENCE: 2520-0101P
CURRENT APPLICATION NUMBER: US/08/605,221
CURRENT FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: HGF-B (five amino acids deletion type)
US-08-605-221-4
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Pred. No. 1.9e
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APPLICANT: MEDICO, Enzo et al.
TITLE OF INVENTION: Recombinant Proteins from HGI
FILE REFERENCE: 0471-0161.P
CURRENT APPLICATION NUMBER: US/09/601,040A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
US-09-601-040A-10
Sequence 2, Application US/09601040A
Patent No. 6730657
GENERAL INFORMATION:
APPLICANT: MEDICO, Enzo et al.
TITLE OF INVENTION: Recombinant Proteins from
FILE REFERENCE: 0471-0161P
CURRENT APPLICATION NUMBER: US/09/601,040A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
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US-09-601-040A-10
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Pred. No. 1.9e-213;
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MSP

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; Sequence 4, Application US/09601040A
; Patent NO. 6730657
; GENERAL INFORMATION:
; APPLICANT: MEDICO, Enzo et al.
; TITLE OF INVENTION: Recombinant Proteins from HGF
; FILE REFERENCE: 0471-0161P
; CURRENT APPLICATION NUMBER: US/09/601,040A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 729
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                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
US-09-601-040A-4
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US-09-601-040A-4
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                                                                                                Query Match
Best Local Similarity
Matches 441; Conserv
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                  QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                   ERKRRNT1HEFKKSAKTTL1KIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
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ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
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                                                                                                99.9%;
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Conservative
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                                                                                                Score 2576; DB 4;
Pred. No. 1.9e-213;
1; Mismatches 0;
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Pred. No. 1.9e-213;
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US-08-030-410-3
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                                                              APPLICATION NUMBER: US/08/030,
APPLICATION NUMBER: 1930521
CLASSIFICATION: 435
ATTORNEY/AGENT IMFORMATION:
ANAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8898
TELECOMMUNICATION INFORMATION:
TELEPAX: (516) 742-4343
TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 3:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kojima, Katsuaki
TITLE OF INVENTION: HEMOPOIETIC
NUMBER OF SEQUENCES: 5
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                                                   SEQUENCE CHARACTERISTICS:
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TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Garden City
STATE: New York
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                                LENGTH:
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Kawano, Genji
Sudo, Tetsuo
Sano, Emiko
                                    723 amino acids
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Nakahata, Tatsutoshi
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US-08-290-937B-3
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APPLICANT: MASUNAGA, HIROKI
APPLICANT: MASUNAGA, HIROKI
APPLICANT: OCGAKI, FUMIKO
APPLICANT: UEDA, MASATSUGU
APPLICANT: HIGASHIO, KANJI
TITLE OF INVENTION: MODIFIED TO
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                               APPLICANT:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                          ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                       STREET: 125 H
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
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Similarity 99.5%;
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                                                                                                                                                                                                                    E: Testa, Hu
125 High St.
                                                                                                                                                                                                                                                                                                                                                                                           MURAKAMI, AKIHIKO
GOTO, MASAAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      SHIMA, NOBUYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                      AMAGUCHI, KYOJI
                                                                                                                                                                                                                                 Hurwitz & Thibeault
                                              US/08/290,937B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2573; DB 3; Pred. No. 3.4e-213;
                                                                                                                                                                                                                                                                                   TCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 723;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 440; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CAMPBEL,
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
TELEFAX: 700 ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                   361
                                                                                                                                        332
                                                                                                                                                                        301
                                                                                                                                                                                                           272
                                                                                                                                                                                                                                            241
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452
                                421
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32
                                                                                                                                                                                                                                                                                                                                                                     WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG
                     PLIPWDYCPISRCEGDTTPTIV 442
                                                                                                                                                          HDMTPENFKCKDLRENYCRNPDGSESFWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG
                                                                                                                                                                                                         HTRWEYCAIKTCADNTMQDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE
                                                                                                                                                                                                                                 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE
                                                                                                                                                                                                                                                                                                    ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK
                                                                   KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN
                                                                                       KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN
                                                                                                                                        HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG
                                                                                                                                                                                                                                                                                                                                                   WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG
                                                                                                                                                                                                                                                                                                                                                                                                                     ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                                                                                                                                                                                                                              ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP
 PLIPWDYCPISRCEGDTTPTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 6.1e-213;
1; Mismatches 1;
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Search completed: October Job time: 1361.31 secs u , 2005, 06:53:49

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